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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.2353 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-2

Perfect score: 584

Sequence: 1 DIYVTSPLSLPVTGPBPAS.....CMQAQSPITFGQGTRELEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	584	100.0	112	7	ADC99773 Anti-huma
2	584	100.0	112	7	ADD05377
3	584	100.0	112	7	ADF09815 Human ant
4	556	95.2	112	8	ADI22130 Anti-plat
5	554	94.9	112	7	ADe28441 Human ant
6	554	94.9	239	7	ADe28465 Human ant
7	553	94.7	112	8	ADI22127 Anti-plat
8	553	94.7	112	8	ADI22112 Anti-plat
9	552	94.5	112	8	ADI22111 Anti-plat
10	552	94.5	112	8	ADI22123 Anti-plat
11	551	94.3	112	8	ADI22124 Anti-plat
12	550	94.2	112	8	AAW53586 Light Cha
13	549.5	94.1	113	8	ADI22126 Anti-plat
14	548	93.8	112	7	ADJ76892 Anti-IGF-
15	548	93.8	112	8	ADI22128 Anti-plat
16	548	93.8	112	8	ADO07297 Human pro
17	548	93.8	113	7	ADJ80417 Hybrid hu
18	548	93.8	113	8	ADP47297 Human pho
19	548	93.8	125	5	ABG76926 Humanised
20	548	93.8	125	8	ADR88410 Human pro
21	546	93.5	112	6	ABR55794 Kappa cha
22	546	93.5	112	6	ABR55786 Kappa cha
23	546	93.5	112	7	ADP03893 Murine-ex
24	545.5	93.4	113	8	ADI22125 Anti-plat
25	545	93.3	112	8	ADI22118 Anti-plat

26	545	93.3	112	8	ADI22129	Adi22129 Anti-plat
27	545	93.3	112	8	ADI22114	Adi22114 Anti-plat
28	545	93.3	112	8	ADL93568	Adl93568 Human CD4
29	545	93.3	238	8	ADL93650	Adl93650 Human CD4
30	544.5	93.2	248	4	AAG65590	Aag65590 Anti-hbDR
31	544	93.2	112	8	ADI22119	Adi22119 Anti-plat
32	543.5	93.1	112	8	ADP47300	Adp47300 Human pho
33	543.5	93.1	113	3	AAV95221	Aay95221 Anti-plat
34	542.5	92.9	111	3	AAV95225	Aay95225 Anti-plat
35	542.5	92.9	112	3	AAV95187	Aay95187 Anti-plat
36	542.5	92.9	113	3	AAV95220	Aay95220 Anti-plat
37	542.5	92.9	114	3	AAV95186	Aay95186 Anti-plat
38	542.5	92.9	131	3	AAV95226	Aay95226 Anti-plat
39	542	92.8	112	7	ADE28487	Ade28487 Human ant
40	542	92.8	112	7	ADE28445	Ade28445 Human ant
41	542	92.8	112	7	ADE28409	Ade28409 Human ant
42	542	92.8	112	7	ADE28425	Ade28425 Human ant
43	542	92.8	112	8	ADI22113	Adi22113 Anti-plat
44	542	92.8	112	8	ADL93580	Adl93580 Human CD4
45	542	92.8	238	8	ADL93654	Adl93654 Human CD4

ALIGNMENTS

RESULT 1
ADC99773
XX ADC99773 standard; protein; 112 AA.

AC ADC99773;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 2.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.

XX Homo sapiens.

XX

PN WO2003057838-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J;

XX

DR WPI; 2003-587113/55.

XX

DR N-PSDB; ADC99775.

XX

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.

XX

PS Claim 3; SEQ ID NO 2; 78pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody comprising
a heavy or light chain amino acid or a heavy or light chain variable
domain where the antibody binds to MUC18. The monoclonal antibody of the
invention demonstrates cytostatic activity and may be useful for treating
a disease or condition associated with the expression of MUC18 on the
cell surface such as tumours, specifically melanoma, oesophageal,
pancreatic or colorectal tumours, carcinomas, particularly cervical
carcinomas and cervical intraepithelial neoplasia and cancers including
colorectal, breast or lung cancer, as well as other malignancies. The
current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 584; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4e-40;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

RESULT 2
 ADD05377 ID ADD05377 standard; protein; 112 AA.
 XX AC ADD05377;
 XX DT 01-JAN-2004 (first entry)
 XX DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 2.
 XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 XX KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 XX OS Homo sapiens.
 XX PN WO2003057006-A2.
 XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041582.
 XX PR 28-DEC-2001; 2001US-0346460P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas J, Bar-Eli M;
 XX WPI; 2003-577496/54.
 XX N-PSDB; ADD05379.

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.

Claim 3; SEQ ID NO 2; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region, protein of the invention.

Sequence 112 AA;
 Query Match 100.0%; Score 584; DB 7; Length 112;

Best Local Similarity 100.0%; Pred. No. 4e-40;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

RESULT 3
 ADF09815 ID ADF09815 standard; protein; 112 AA.
 XX AC ADF09815;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human anti-MUC18 monoclonal antibody light chain #1.
 XX KW cell proliferation inhibition; MUC18 tumour antigen;
 XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 XX KW carcinoma; cancer; malignancy; light chain; human.
 XX OS Homo sapiens.
 XX PN WO2003057837-A2.
 XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041580.
 XX PR 28-DEC-2001; 2001US-0346414P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas J;
 XX WPI; 2003-598367/56.
 XX N-PSDB; ADF09817.

Inhibiting cell proliferation associated with expression of MUC18 tumour antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

Claim 3; SEQ ID NO 2; 83pp; English.

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific monoclonal antibody.

Sequence 112 AA;
 Query Match 100.0%; Score 584; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4e-40;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
CC clotting. The present sequence is used in the exemplification of the
CC present invention.

XX
SQ Sequence 112 AA;

Query Match 95.2%; Score 556; DB 8; Length 112;
Best Local Similarity 94.6%; Pred. No. 7.6e-38;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVVTQSPISLPVTPGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLGSRNA 60
DB 1 DIVVTQSPISLPVTPGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLGSRNA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQDSPTFGQGRLDI 111
DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQDSPTFGQGRLDI 111

RESULT 5
ADE28441
ID ADE28441 standard; protein; 112 AA.
XX AC ADE28441;
XX AC ADE28441;
DT 29-JAN-2004 (first entry)
XX DE Human anti-CD40 antibody 21-4-1 full length light chain protein.
XX KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX KW human; light chain; 21-4-1.
OS Homo sapiens.
XX PN WO2003040170-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036107.
XX PR 09-NOV-2001; 2001US-0348980P.
XX PA (PFIZ) PFIZER PROD INC.
XX PA (ABGE-) ABGENIX INC.
XX PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX WPI; 2003-441521/41.
XX DR N-PSDB; ADE28440.
XX PT New chimeric or human monoclonal antibody or its antigen-binding portion
XX PT that specifically binds to and activates human CD40, useful for enhancing
XX PT an immune response in a human, or treating cancer, HIV, neutropenia or
XX PT viral infections.
XX PS Claim 7; SEQ ID NO 48; 177pp; English.
XX CC The invention relates to a novel chimeric or human monoclonal antibody or
XX CC its antigen-binding portion that specifically binds to and activates
XX CC human CD40. The anti-CD40 antibody of the invention demonstrates
XX CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX CC activities and may be useful for treating a hyperproliferative disorder
XX CC such as cancer, viral and bacterial infection or genetic, primary or
XX CC combined immunodeficiency conditions including neutropenia or HIV
XX CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX CC in a biological sample in vitro or in vivo, as well as during gene
XX CC therapy procedures. The current sequence is that of the human anti-CD40
XX CC antibody full length light chain protein of the invention.

XX
SQ Sequence 112 AA;

RESULT 4
ADI22130
ID ADI22130 standard; protein; 112 AA.
XX AC ADI22130;
XX AC ADI22130;
DT 22-APR-2004 (first entry)
XX DE Anti-platelet autoantibody related light chain amino acid L54 SEQ:93.
XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
XX KW thrombus; platelet adhesion inhibition;
XX KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
XX KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
XX KW thrombolytic; human.
OS Homo sapiens.
OS Synthetic.
XX PN WO2004005890-A2.
XX PD 15-JAN-2004.
XX PF 03-JUL-2003; 2003WO-US021304.
XX PR 03-JUL-2002; 2002US-0394352P.
XX PR 18-SEP-2002; 2002US-0411694P.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX WPI; 2004-142998/14.
XX DR N-PSDB; ADI22077.
XX PS Claim 12; SEQ ID NO 93; 232pp; English.
XX CC The present invention describes a method (M1) for identifying an anti-
XX CC platelet autoantibody (I) in a mammal. The autoantibody is detected by
XX CC producing an antibody phage display library from B-lymphocytes obtained
XX CC from the mammal, and screening the library to detect a phage that
XX CC specifically binds with a platelet component, where the screening
XX CC comprises panning the phage on intact platelets using competitive cell-
XX CC surface panning. Also described: (1) an autoantibody identified by (M1);
XX CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
XX CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
XX CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
XX CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
XX CC (M4) binding of an anti-platelet autoantibody with a platelet component;
XX CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
XX CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
XX CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
XX CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
XX CC anti-platelet autoantibody, or its biologically active fragment with a
XX CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
XX CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
XX CC the method of (12); (14) a peptide that specifically binds with an anti-
XX CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
XX CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
XX CC clotting, inhibiting platelet aggregation, inhibiting platelet function
XX CC or inhibiting platelet activation comprising an amount of an anti-
XX CC platelet autoantibody, or its biologically active fragment that
XX CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
XX CC its fragment comprises an antigen binding region derived from an H414
XX CC anti-platelet autoantibody; the kit further comprising a peptide
XX CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
XX CC and an instructions for use. (I) has haemostatic, anticoagulant and
XX CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
XX CC and for developing therapeutics for diseases mediated by autoantibody
XX CC binding with platelet antigens. (M6) and (M12) are useful for treating
XX CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic

Query Match 94.9%; Score 554; DB 7; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.1e-37;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLPKQPSPHLLIYLGNSRA 60
|||||
DB 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLPKQPSPHLLIYLGNSRA 60
|||||

QY 61 SGVPDRFSGSGDFTFLKISRVEADVGVYCYCMAQOQSPITFGQGTLEIK 112
|||||
DB 61 SGVPDRFSGSGDFTFLKISRVEADVGVYCYCMAQOQSPITFGQGTLEIK 112
|||||

RESULT 6
ADE28465
ID ADE28465 standard; protein; 239 AA.
XX
AC ADE28465;
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 23-28-1 full length light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; 23-28-1.
XX
OS Homo sapiens.
XX
PN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PRIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
XX WPI; 2003-441521/41.
DR N-PSDB; ADE28464.
XX
XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
PS Claim 7; SEQ ID NO 72; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody full length light chain protein of the invention.
XX
SQ Sequence 239 AA;

Query Match 94.9%; Score 554; DB 7; Length 239;
Best Local Similarity 94.6%; Pred. No. 2.3e-37;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLPKQPSPHLLIYLGNSRA 60
|||||

Db 21 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLPKQPSPHLLIYLGNSRA 80
QY 61 SGVPDRFSGSGDFTFLKISRVEADVGVYCYCMAQOQSPITFGQGTLEIK 112
|||||
Db 81 SGVPDRFSGSGDFTFLKISRVEADVGVYCYCMAQOQSPITFGQGTLEIK 132
|||||

RESULT 7
ADI22127
ID ADI22127 standard; protein; 112 AA.
XX
AC ADI22127;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-platelet autoantibody related light chain amino acid L51 SEQ:90.
XX
KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN WO2004005890-A2.
XX
PD 15-JAN-2004.
XX
XX 03-JUL-2003; 2003WO-US021304.
PF
XX 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
DR WPI; 2004-142998/14.
DR N-PSDB; ADI22074.
XX
PS Claim 12; SEQ ID NO 90; 232pp; English.
XX
XX The present invention describes a method (M1) for identifying an anti-
CC platelet autoantibody (I) in a mammal. The autoantibody is detected by
CC producing an antibody phage display library from B-lymphocytes obtained
CC from the mammal, and screening the library to detect a phage that
CC specifically binds with a platelet component, where the screening
CC comprises panning the phage on intact platelets using competitive cell-
CC surface panning. Also described: (1) an autoantibody identified by (M1);
CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
CC (M4) binding of an anti-platelet autoantibody with a platelet component;
CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
CC anti-platelet autoantibody, or its biologically active fragment with a
CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
CC the method of (12); (14) a peptide that specifically binds with an anti-
CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
CC clotting, inhibiting platelet activation, inhibiting platelet function
CC or inhibiting platelet activation comprising an amount of an anti-
CC platelet autoantibody, or its biologically active fragment that
CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
CC its fragment comprises an antigen binding region derived from an H44L4
CC anti-platelet autoantibody, the kit further comprising a peptide
CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator

CC and an instructions for use. (I) has haemostatic, anticoagulant and
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
 CC and for developing therapeutics for diseases mediated by autoantibody
 CC binding with platelet antigens. (M6) and (M12) are useful for treating
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
 CC clotting. The present sequence is used in the exemplification of the
 CC present invention.

XX SQ Sequence 112 AA;

Query Match 94.7%; Score 553; DB 8; Length 112;
 Best Local Similarity 94.6%; Pred. No. 1.3e-37;
 Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLVPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPHLLIYLGSHRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSPITFGQGRLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSPITFGQGRLEIK 112

RESULT 8

AD122112

ID AD122112 standard; protein; 112 AA.

XX AC AD122112;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L36 SEQ.75.

XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;

XX KW thrombus; platelet adhesion inhibition;

XX KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;

XX KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;

XX KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO2004005890-A2.

XX XX 15-JAN-2004.

XX XX 03-JUL-2003; 2003WO-US021304.

XX XX 03-JUL-2002; 2002US-0394352P.

XX XX 18-SEP-2002; 2002US-0411694P.

XX XX (UYPE-) UNIV PENNSYLVANIA.

XX XX Siegel DL;

XX XX WPI; 2004-142998/14.

XX XX N-PSDB; AD122059.

XX XX Claim 12; SEQ ID NO 75; 232pp; English.

CC The present invention describes a method (M1) for identifying an anti-
 CC platelet autoantibody (I) in a mammal. The autoantibody is detected by
 CC producing an antibody phage display library from B-lymphocytes obtained
 CC from the mammal, and screening the library to detect a phage that
 CC specifically binds with a platelet component, where the screening
 CC comprises panning the phage on intact platelets using competitive cell-
 CC surface panning. Also described: (1) an autoantibody identified by (M1);
 CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
 CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
 CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
 CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
 CC (M4) binding of an anti-platelet autoantibody with a platelet component;

CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
 CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
 CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
 CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
 CC anti-platelet autoantibody, or its biologically active fragment with a
 CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
 CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
 CC the method of (12); (14) a peptide that specifically binds with an anti-
 CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
 CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
 CC clotting, inhibiting platelet aggregation, inhibiting platelet function
 CC or inhibiting platelet activation comprising an amount of an anti-
 CC platelet autoantibody, or its biologically active fragment that
 CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
 CC its fragment comprises an antigen binding region derived from an H44L4
 CC anti-platelet autoantibody, the kit further comprising a peptide
 CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
 CC and an instructions for use. (I) has haemostatic, anticoagulant and
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
 CC and for developing therapeutics for diseases mediated by autoantibody
 CC binding with platelet antigens. (M6) and (M12) are useful for treating
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
 CC clotting. The present sequence is used in the exemplification of the
 CC present invention.

XX SQ Sequence 112 AA;

Query Match 94.7%; Score 553; DB 8; Length 112;
 Best Local Similarity 94.6%; Pred. No. 1.3e-37;
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLVPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSPITFGQGRLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSPITFGQGRLEIK 112

RESULT 9

AD122111

ID AD122111 standard; protein; 112 AA.

XX AC AD122111;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L35 SEQ.74.

XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;

XX KW thrombus; platelet adhesion inhibition;

XX KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;

XX KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;

XX KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO2004005890-A2.

XX XX 15-JAN-2004.

XX XX 03-JUL-2003; 2003WO-US021304.

XX XX 03-JUL-2002; 2002US-0394352P.

XX XX 18-SEP-2002; 2002US-0411694P.

XX XX (UYPE-) UNIV PENNSYLVANIA.

XX XX Siegel DL;

DR WPI; 2004-142998/14.
 DR N-PSDB; ADI22058.
 XX
 PS Claim 12; SEQ ID NO 74; 232pp; English.
 CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 112 AA;
 Query Match 94.5%; Score 552; DB 8; Length 112;
 Best Local Similarity 94.6%; Pred. No. 1.6e-37;
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGVNYLDWYLOKPGQSPHLLIYLSNRA 60
 DB 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGVNYLDWYLOKPGQSPHLLIYLSNRA 60
 QY 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCMQAQSPITFGGQTRLEIK 112
 DB 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCMQAQSPITFGGQTRLEIK 112

RESULT 10
 ADI22123
 ID ADI22123 standard; protein; 112 AA.
 XX
 AC ADI22123;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Anti-platelet autoantibody related light chain amino acid L47 SEQ:86.
 KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
 KW thrombus; platelet adhesion inhibition;
 KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
 KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
 KW thrombolytic; human.

XX Homo sapiens.
 OS Synthetic.
 XX WO2004005890-A2.
 XX 15-JAN-2004.
 XX 03-JUL-2003; 2003WO-US021304.
 XX 03-JUL-2002; 2002US-0394352P.
 XX 18-SEP-2002; 2002US-0411694P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel Du;
 XX WPI; 2004-142998/14.
 DR N-PSDB; ADI22070.
 DR
 PS Claim 12; SEQ ID NO 86; 232pp; English.
 CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 112 AA;
 Query Match 94.5%; Score 552; DB 8; Length 112;
 Best Local Similarity 95.5%; Pred. No. 1.6e-37;
 Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGVNYLDWYLOKPGQSPHLLIYLSNRA 60
 DB 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGVNYLDWYLOKPGQSPHLLIYLSNRA 60
 QY 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCMQAQSPITFGGQTRLEIK 112
 DB 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCMQAQSPITFGGQTRLEIK 112

RESULT 11
ADI22124
ID ADI22124 standard; protein; 112 AA.
XX
AC ADI22124;
XX
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-platelet autoantibody related light chain amino acid L48 SEQ:87.
XX
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO2004005890-A2.
XX
XX 15-JAN-2004.
XX
XX 03-JUL-2003; 2003WO-US021304.
XX
XX 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX Siegel DL;
PI
XX WPI: 2004-142998/14.
DR N-PSDB; ADI22071.
XX
XX
PS Claim 12; SEQ ID NO 87; 232pp; English.
XX
XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic

CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.
CC
XX
SQ Sequence 112 AA;
Query Match 94.3%; Score 551; DB 8; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-37;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
DB 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQSPITFGQGRLEIK 112
DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQSPITFGQGRLEIK 112
RESULT 12
AAW53586
ID AAW53586 standard; protein; 112 AA.
XX
AC AAW53586;
XX
DT 23-JUL-1998 (first entry)
XX
DE Light chain of a human antibody.
XX
KW Light chain; human; humanised immunoglobulin; NOK2; Fas ligand;
KW inhibition; apoptosis; Fas expression; treatment; AIDS; rejection;
KW transplant surgery; autoimmune disease; SLE; RA; diabetes.
XX
XX Homo sapiens.
XX
XX WO9810070-A1.
XX
XX 12-MAR-1998.
XX
XX 27-AUG-1997; 97WO-JP002983.
XX
XX 02-SEP-1996; 96JP-00231742.
PR 20-SEP-1996; 96JP-00271546.
XX
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX Okumura K, Nakata M, Higuchi H, Ushio Y, Maeda H, Eda Y;
XX WPI: 1998-193620/17.
XX
XX Human immunoglobulin or its active fragment specific for Fas ligand - for treatment of AIDS, organ rejection, autoimmune diseases e.g. systemic lupus erythematosus and diabetes.
XX
XX Disclosure; Page 261; 348pp; Japanese.
XX
XX The present sequence represents the light chain of a human antibody, and can be used in the humanised immunoglobulin of the invention. The humanised immunoglobulin reacts specifically with a region of a Fas ligand that is important in inhibiting apoptosis induced by cells with Fas expression. The immunoglobulin of the invention can inhibit physiological reactions between a Fas ligand and Fas, typified by apoptosis. The humanised immunoglobulin is used for treatment of AIDS, rejection following transplant surgery, autoimmune diseases such as SLE or RA, and diabetes
XX
XX Sequence 112 AA;
Query Match 94.2%; Score 550; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.3e-37;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQOSPIITFGQGTTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQALQTPVTFGQGTTRLEIK 112

RESULT 13

ID ADI22126 standard; protein; 113 AA.
XX ADI22126;
XX AC ADI22126;
XX DT 22-APR-2004 (first entry)
XX Anti-platelet autoantibody related light chain amino acid I50 SEQ:89.
DE anti-platelet autoantibody; autoantibody; blood clotting inhibition;
XX thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human.
XX Homo sapiens.
OS Synthetic.
XX WO2004005890-A2.
XX 15-JAN-2004.
XX 03-JUL-2003; 2003WO-US021304.
XX 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2004-142998/14.
DR N-PSDB; ADI22073.
XX Claim 12; SEQ ID NO 89; 232pp; English.
XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide

CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 113 AA;

Query Match 94.1%; Score 549.5; DB 8; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.6e-37;
Matches 107; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQOS-PITFGQGTTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQALQTPVTFGQGTTRLEIK 113

RESULT 14

ADJ76892
ID ADJ76892 standard; protein; 112 AA.
XX AC ADJ76892;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #9.
XX cytotstatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX Homo sapiens.
XX WO2003059951-A2.
XX 24-JUL-2003.
XX 20-JAN-2003; 2003WO-FR000178.
PR 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
XX Disclosure; SEQ ID NO 58; 164pp; French.
XX The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit

CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX Sequence 112 AA;

Query Match 93.8%; Score 548; DB 7; Length 112;
 Best Local Similarity 93.8%; Pred. No. 3.4e-37;
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIWMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

DB 1 DIWMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVVYCMQAQSPITFGQGLRLEIK 112

DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVVYCMQAQSPITFGQGLRLEIK 112

RESULT 15

AD122128
 ID AD122128 standard; protein; 112 AA.

XX AC AD122128;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L52 SEQ:91.

XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
 KW thrombus; platelet adhesion inhibition;
 KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
 KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
 KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004005890-A2.

XX PD 15-JAN-2004.

XX PF 03-JUL-2003; 2003WO-US021304.

XX PR 03-JUL-2002; 2002US-0394352P.

XX PR 18-SEP-2002; 2002US-0411694P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2004-142998/14.

XX DR N-PSDB; AD122075.

XX PS Claim 12; SEQ ID NO 91; 232bp; English.

XX CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)

CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
 CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
 CC anti-platelet autoantibody, or its biologically active fragment with a
 CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
 CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
 CC the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
 CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
 CC clotting, inhibiting platelet aggregation, inhibiting platelet function
 CC or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that
 CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
 CC its fragment comprises an antigen binding region derived from an H44L4
 CC anti-platelet autoantibody, the kit further comprising a peptide
 CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
 CC and an instructions for use. (I) has haemostatic, anticoagulant and
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
 CC and for developing therapeutics for diseases mediated by autoantibody
 CC binding with platelet antigens. (M6) and (M12) are useful for treating
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
 CC clotting. The present sequence is used in the exemplification of the
 CC present invention.

XX SQ Sequence 112 AA;

Query Match 93.8%; Score 548; DB 8; Length 112;

Best Local Similarity 93.8%; Pred. No. 3.4e-37;

Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIWMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

DB 1 DIWMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVVYCMQAQSPITFGQGLRLEIK 112

DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVVYCMQAQSPITFGQGLRLEIK 112

Search completed: November 16, 2005, 21:51:35

Job time : 66.2353 secs

(CASE) XIN/TO FORTI SHAL

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.3824 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-2

Perfect score: 584

Sequence: 1 DIWVTOSPLSLPVTGPGEAS.....CMQAQSPITFGQGTLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	93.8	112	2 S58207	Ig light chain V r
2	548	93.8	132	2 S26882	Ig kappa chain V r
3	548	93.8	135	2 S40342	Ig kappa chain - h
4	548	93.8	136	2 S40357	Ig kappa chain V-J
5	542	92.8	112	2 S58206	Ig light chain V r
6	536	91.8	117	1 K2HUGM	Ig kappa chain pre
7	536	91.8	125	2 S40356	Ig kappa chain - h
8	527.5	90.3	126	2 S40339	Ig kappa chain - h
9	525	89.9	123	1 K2HUTW	Ig kappa chain V-I
10	517	88.5	121	2 S40371	Ig kappa chain - h
11	514	88.0	131	2 S40372	Ig kappa chain V-J
12	499.5	85.5	112	1 K2HUMH	Ig kappa chain V-I
13	497.5	85.2	123	2 S40319	Ig kappa chain - h
14	488	83.6	100	2 S24681	Ig kappa chain - h
15	487	83.4	124	2 S03876	Ig kappa chain V-I
16	474.5	81.2	114	2 S40375	Ig kappa chain - h
17	471.5	80.7	130	2 S40321	Ig kappa chain - h
18	469	80.3	113	1 K2HUPR	Ig kappa chain V-I
19	464.5	79.5	115	1 K2HUCM	Ig kappa chain V-I
20	459.5	78.7	140	2 S22658	Ig kappa chain pre
21	458	78.4	142	2 S22902	Ig kappa chain V r
22	454	77.7	112	2 S38719	Ig light chain V r
23	454	77.7	112	2 F27887	Ig kappa chain V r
24	453	77.6	113	2 PL0203	anti-DNA autoantib
25	453	77.6	126	2 S40312	Ig kappa chain - h
26	452	77.4	131	2 B39276	Ig light chain pre
27	452	77.4	133	2 S23230	Ig kappa chain pre
28	452	77.4	219	2 S52028	Ig kappa chain - m
29	449.5	77.0	114	2 S40340	Ig kappa chain V-J

RESULT 1

S58207

Ig light chain V region anti-F(ab')2 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000

C;Accession: S58207

R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebl, S.; Bretling, I

submitted to the EMBL Data Library, July 1995

A;Description: Characterization of heavy and light chain immunoglobulin variable region

A;Reference number: S58206

A;Accession: S58207

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEL>

A;Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 112;

Best Local Similarity 93.8%; Pred.No. 4.5e-42;

Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIWVTOSPLSLPVTGPGEASISCRSSQSLHSGYNYLDWYLOKPGOSPHLLIYLGSNRA 60

Db 1 DIWVTOSPLSLPVTGPGEASISCRSSQSLHSGYNYLDWYLOKPGOSPHLLIYLGSNRA 60

Qy 61 SGVPDRPFGSGSGTDFTLKISRVEADVGYYVCMAQOQSPITFGQGTLEIK 112

Db 61 SGVPDRPFGSGSGTDFTLKISRVEADVGYYVCMAQOQSPITFGQGTLEIK 112

RESULT 2

S26882

Ig kappa chain V region (V607) - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C;Accession: S26882

R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.

Nature 347, 90-92, 1990

A;Title: Megabase inversions in the human genome as physiological events.

A;Reference number: S26882; MUID:90370099; PMID:2118596

A;Accession: S26882

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-132 <WEI>

A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1333367

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 132;
Best Local Similarity 93.8%; Pred. No. 5.3e-42;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60
Db 21 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 132

RESULT 3
S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:G441372; PID:G441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 135;
Best Local Similarity 93.8%; Pred. No. 5.5e-42;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60
Db 14 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 73

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112
Db 74 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 125

RESULT 4
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 136;
Best Local Similarity 93.8%; Pred. No. 5.5e-42;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60
Db 21 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 132

RESULT 5
S58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58206
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, I.
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58206
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89054; NID:G929640; PIDN:CAA61441.1; PID:G929641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 542; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.5e-41;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112

RESULT 6
K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506; PMID:6325927
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Cross-references: UNIPROT:P06309
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:I36265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted

Query Match 91.8%; Score 536; DB 1; Length 117;
Best Local Similarity 92.0%; Pred. No. 5.5e-41;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 60
Db 5 DIVMTQSPFLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLRKPGQSPHLLIYLGSNRA 64

QY 61 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQAQQSPITFGQGTREIK 112
 |||
 Db 65 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQGLQTPQTFGQGTREIK 116
 |||

RESULT 7

S40356
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 R:Putnam, F.W.; Whitely Jr., E.J.; Paul, C.; Davidson, J.N.
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40356
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-125 <KLE>
 A:CROSS-references: EMBL:X72449; NID:G441366; PIDN:CAA51117.1; PID:G441367
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 536; DB 2; Length 125;
 Best Local Similarity 91.1%; Pred. No. 5.9e-41;
 Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRNGNYLDWYKQPSPLLIYLSNRA 60
 |||

Db 10 DIVMTQSPSLPVTGPEPASISCRSSQSLRHNGNYLDWYKQPSPLLIYLSNRA 69
 |||

QY 61 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQAQQSPITFGQGTREIK 112
 |||

Db 70 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQVLIPLIFGGTKVEIK 121
 |||

RESULT 8

S40339
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40339
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-126 <KLE>
 A:CROSS-references: EMBL:X72449; NID:G441366; PIDN:CAA51117.1; PID:G441367
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:31-110/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 527.5; DB 2; Length 126;
 Best Local Similarity 92.0%; Pred. No. 3.4e-40;
 Matches 103; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRNGNYLDWYKQPSPLLIYLSNRA 60
 |||

Db 16 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGNYLDWYKQPSPLLIYLSNRA 75
 |||

QY 61 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQAQQSPITFGQGTREIK 112
 |||

Db 76 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQALQ-PWTFGQGTVEIK 126
 |||

RESULT 9

K2HUTW
 Ig kappa chain V-II region (Tew) - human (tentative sequence)
 C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A90370; A92764; A01888
 R:Putnam, F.W.; Whitely Jr., E.J.; Paul, C.; Davidson, J.N.
 Biochemistry 12, 3763-3780, 1973
 A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloid
 A:Reference number: A90370; MUID:74148480; PMID:4596149
 A:Contents: Bence Jones protein Tew
 A:Accession: A90370
 A:Molecule type: protein
 A:Residues: 1-113 <PUT>
 A:CROSS-references: UNIPROT:P01617
 A:Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia;
 A:Note: the C region of this chain has the Inv (1,2) marker
 R:Terrey, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osseman, E.F.; Glenner, G.G.
 J. Clin. Invest. 52, 1276-1281, 1973
 A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with
 A:Reference number: A92764; MUID:73166638; PMID:4700495
 A:Contents: amyloid protein Tew
 A:Accession: A92764
 A:Molecule type: protein
 A:Residues: 1-27 <TER>
 A:Note: the major amyloid protein appears to be identical with the Bence Jones protein in
 C:Genetics:
 A:Gene: GDB:IGKV2
 A:CROSS-references: GDB:136265
 A:Map position: 2p12-2p12
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la;
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: amyloid; heterotetramer; immunoglobulin
 F:16-95/Domain: immunoglobulin homology <IMM>
 F:23-93/Disulfide bonds: #status predicted

Query Match 89.9%; Score 525; DB 1; Length 113;
 Best Local Similarity 90.2%; Pred. No. 5.1e-40;
 Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRNGNYLDWYKQPSPLLIYLSNRA 60
 |||

Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRHSDGFDLWYKQPSPLLIYLSNRA 60
 |||

QY 61 SGVPRFSGSGGTDTLTKISRVEADVGVYCMQAQQSPITFGQGTREIK 112
 |||

Db 61 SGVPRFSGSGGTDTLTKISRVEADVGVYCMALQAPITFGQGTREIK 112
 |||

RESULT 10

S40371
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40371
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-121 <KLE>
 A:CROSS-references: EMBL:X72481; NID:G441430; PIDN:CAA51149.1; PID:G441431
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 517; DB 2; Length 121;
 Best Local Similarity 90.8%; Pred. No. 2.8e-39;
 Matches 99; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 MTQSPSLPVTGPEPASISCRSSQSLRNGNYLDWYKQPSPLLIYLSNRA 63
 |||

Db 1 MTQSPSLPVTGPEPASISCRSSQSLLYSTGYLDWYKQPSPLLIYLSNRA 60
 |||

```
QY 64 PDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSPITFGQGTGLEIK 112
|||||
Db 61 PDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQGLQPTTFFGQGTGLEIK 109
|||||

RESULT 11
S40372
IG kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40372
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40372; MUID:94080891; PMID:8258341
A;Accession: S40372
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-131 <KLE>
A;Cross-references: EMBL:X72482; NID:G441432; PIDN:CAA51150.1; PID:G441433
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 514; DB 2; Length 131;
Best Local Similarity 88.3%; Pred. No. 5.7e-39;
Matches 98; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60
|||||
Db 21 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSTRA 80
|||||

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSPITFGQGTGLEI 111
|||||
Db 81 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQPLQPTTFFGQGTGLEI 131
|||||

RESULT 12
K2HUML
IG kappa chain V-II region (MIL) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01887
R;Dreyer, W.J.; Gray, W.R.; Hood, L.
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967
A;Title: The genetic, molecular, and cellular basis of antibody formation: some facts and
A;Reference number: A01887
A;Accession: A01887
A;Molecule type: protein
A;Residues: 1-112 <DRE>
A;Cross-references: UNIPROT:P01616
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 85.5%; Score 499.5; DB 1; Length 112;
Best Local Similarity 82.1%; Pred. No. 9.5e-38;
Matches 92; Conservative 14; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60
|||||
Db 1 DIVLTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 59
|||||

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSPITFGQGTGLEIK 112
|||||
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Db 60 SGVDPFRFSGSGGTDTFTLKISRVAZBVGVCYCMQALQPTPLTFGGGTNVEIK 111
|||||

RESULT 13
S40319
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40319
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40319
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72429; NID:G441326; PIDN:CAA51097.1; PID:G441327
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-105/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 497.5; DB 2; Length 123;
Best Local Similarity 89.7%; Pred. No. 1.6e-37;
Matches 96; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60
|||||
Db 11 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 70
|||||

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSP-ITFGOG 106
|||||
Db 71 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQALQPTPSVTSAGK 117
|||||

RESULT 14
S24681
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S24681
R;van Es, J.H.
submitted to the EMBL Data Library, July 1992
A;Reference number: S24679
A;Accession: S24681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <VAN>
A;Cross-references: EMBL:X67904; NID:G33435; PIDN:CAA48102.1; PID:G33436
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 488; DB 2; Length 100;
Best Local Similarity 94.0%; Pred. No. 8.9e-37;
Matches 94; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60
|||||
Db 1 DIVMTQSPISLPVTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60
|||||

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSP 100
|||||
Db 61 SGVDPFRFSGSGGTDTFTLKISRVEAEDVGYVYCMQALQTP 100
|||||

RESULT 15
S03876
IG kappa chain V-II region (Inc) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S03876
```

R:Perri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
 Biochim. Biophys. Acta 995, 103-108, 1989
 A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
 A:Reference number: S03876; MUID:89194238; PMID:2495028
 A:Accession: S03876
 A:Molecule type: protein
 A:Residues: 1-124 <PER>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match	83.4%	Score 487;	DB 2;	Length 124;
Best Local Similarity	83.0%	Pred. No. 1.4e-36;		
Matches	93;	Conservative 9;	Mismatches 10;	Indels 0; Gaps 0;

QY	1	DIVMTQSP	PLSLPVT	PGEPASIS	CRSSQS	LLRSGNY	LDWY	LQKPGQ	SPHLLI	YLG	SNRA	60
Db	1	DIVLTQSP	LSLPVT	PGEPASIS	CKSSQS	SLMHSSG	NDWY	LQKPGQ	SPQIV	IYLG	SNRA	60

QY	61	SGVPRF	SGSGG	TDFTL	KISR	VEAD	VGYY	CMQA	QSPIT	FGQ	TRLEIK	112
Db	61	SGVPTD	FGSGG	TDFTL	LISV	GAED	VGYY	CMQA	LQTP	WTFG	QGT	KVGIK 112

Search completed: November 16, 2005, 22:04:06
 Job time : 14.3824 secs

1944 JAN 10 10 10 AM

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 62.7941 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-2
Perfect score: 584
Sequence: 1 DIVWQSLSLPVTGEPAS.....CMQAQSPITFGQTRLEIK 112

Scoring table: .BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	91.8	117	1 KV2E_HUMAN	P06309 homo sapien
2	535	91.6	239	2 Q8NEK0	Q8NEK0 homo sapien
3	525	89.9	113	1 KV2D_HUMAN	P01617 homo sapien
4	519.5	89.0	240	2 Q6PIH6	Q6PIH6 homo sapien
5	499.5	85.5	112	1 KV2C_HUMAN	P01616 homo sapien
6	469	80.3	113	1 KV2E_HUMAN	P01615 homo sapien
7	464.5	79.5	115	1 KV2A_HUMAN	P01614 homo sapien
8	450	77.1	248	2 Q6S2Q7	Q6S2Q7 mus sp. b3(
9	447	76.5	239	2 Q6P491	Q6P491 homo sapien
10	446	76.4	239	2 Q8TCD0	Q8TCD0 homo sapien
11	444	76.0	133	1 KV2F_HUMAN	P06310 homo sapien
12	437	74.8	113	1 KV2G_MOUSE	P01631 mus musculus
13	428.5	73.4	114	2 Q9UL80	Q9UL80 homo sapien
14	428	73.3	219	2 Q6S2C0	Q6S2C0 mus musculus
15	420	71.9	113	1 KV2F_MOUSE	P01630 mus musculus
16	418	71.6	112	1 KV2D_MOUSE	P01629 mus musculus
17	416	71.2	113	1 KV2E_MOUSE	P01976 mus musculus
18	415.5	71.1	108	1 KV1_CANFA	P01618 canis famil
19	405	69.3	112	2 Q6LEM8	Q6LEM8 mus musculus
20	405	69.3	113	1 KV2C_MOUSE	P01628 mus musculus
21	399	68.3	112	1 KV2A_MOUSE	P01626 mus musculus
22	389.5	66.7	114	1 KV4A_HUMAN	P01625 homo sapien
23	381.5	65.3	134	1 KV4C_HUMAN	P06314 homo sapien
24	378.5	64.8	255	2 Q6K805	Q6K805 mus musculus
25	374	64.0	109	1 KV3D_HUMAN	P01622 homo sapien
26	372	63.7	129	1 KV3L_HUMAN	P18135 homo sapien
27	371	63.5	109	2 Q9UL78	Q9UL78 homo sapien
28	371	63.5	133	1 KV4B_HUMAN	P06313 homo sapien
29	369	63.2	120	1 KV2E_MOUSE	P01627 mus musculus
30	367	62.8	109	1 KV3B_HUMAN	P01620 homo sapien
31	367	62.8	129	1 KV3M_HUMAN	P18136 homo sapien

32	365.5	62.6	111	1 KV3S_MOUSE	P01671 mus musculus
33	365.5	62.6	236	2 Q6PIL8	Q6PIL8 homo sapien
34	364.5	62.4	111	1 KV3U_MOUSE	P01673 mus musculus
35	364	62.3	108	1 KV3A_HUMAN	P01619 homo sapien
36	363.5	62.2	111	2 Q920E9	Q920E9 mus musculus
37	361.5	61.9	111	1 KV3R_MOUSE	P01670 mus musculus
38	359	61.5	109	1 KV3E_HUMAN	P01623 homo sapien
39	359	61.5	109	1 KV3G_HUMAN	P04206 homo sapien
40	358	61.3	235	2 Q6GMV9	Q6GMV9 homo sapien
41	355.5	60.9	111	1 KV3M_MOUSE	P01665 mus musculus
42	354.5	60.7	111	1 KV3N_MOUSE	P01666 mus musculus
43	354.5	60.7	111	1 KV3T_MOUSE	P01672 mus musculus
44	354	60.6	109	1 KV3F_HUMAN	P01624 homo sapien
45	353.5	60.5	109	1 KV4D_HUMAN	P83593 homo sapien

ALIGNMENTS

RESULT 1
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 200009; -; NOT_ANNOTATED_CDS.
CC FIR; A01889; K2HUGM.
CC HSSP; Q99M37; 1191.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.
FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E559B1 CRC64;

Query Match 91.8%; Score 536; DB 1; Length 117;
Best Local Similarity 92.0%; Pred. No. 5.1e-48;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 5 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 64
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 112
DB 65 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 116

RESULT 2
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Tkatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AA030814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSP; P01834; I17Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_YHC; UNKNOWN_1.
KW Hypothetical protein.

QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 5 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 64
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 112
DB 65 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 116

Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 21 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 80
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 112
DB 81 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 132

RESULT 3
KV2D HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -I- MISCELLANEOUS: The major amyloid protein appears to be identical
with the Bence Jones protein isolated from the same patient.
CC -I- MISCELLANEOUS: This protein was isolated from the urine of a
patient with plasma cell dyscrasia and amyloidosis.
CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
DR PIR; A90370; K2HUTW.
DR HSP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 0C3C38F81F1843CA CRC64;
Query Match 89.9%; Score 525; DB 1; Length 113;
Best Local Similarity 90.2%; Pred. No. 6.9e-47;
Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 5 DIVMTQSLPLVPTGPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 64
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 112
DB 65 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCMQAOQSPITPGQGTREIK 116


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Db 1 DIVMTOSPLSLPVTGPEPASISCRSSQSLHSDGDFLWYLYLQKPGQSPZLLIYLSNRA 60
QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMQAQQSPITFGQGTREIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMZALQAPITFGQGTREIK 112

RESULT 4
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleks U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188B4DB8B781EC4 CRC64;

Query Match 89.0%; Score 519.5; DB 2; Length 240;
Best Local Similarity 90.3%; Pred. No. 6.3e-46;
Matches 102; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVMTOSPLSLPVTGPEPASISCRSSQSLHSDGDFLWYLYLQKPGQSPZLLIYLSNRA 60
Db 21 DIVMAQSPLSLVTGPEPASISCRSSQSLHSDGDFLWYLYLQKPGQSPZLLIYLSNRA 80
QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMQAQQSPITFGQGTREIK 112
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Db 81 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMQAQQSPITFGQGTREIK 133

RESULT 5
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID KV2C_HUMAN
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis."
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367 (1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 85.5%; Score 499.5; DB 1; Length 112;
Best Local Similarity 82.1%; Pred. No. 3.1e-44;
Matches 92; Conservative 14; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTOSPLSLPVTGPEPASISCRSSQSLHSDGDFLWYLYLQKPGQSPZLLIYLSNRA 60
Db 1 DIVLTSPLSLPVTGPEPASISCRSSQSLHSDGDFLWYLYLQKPGQSPZLLIYLSNRA 59
QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMQAQQSPITFGQGTREIK 112
Db 60 SGVPRFSGSGGTDFTLKISRVEADVGVYVYCMQAQQSPITFGQGTREIK 111

RESULT 6
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riessen W.F., Jatton J.-C.;
```

"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
DR PIR; A01886; K2HUF8.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39B46DB96BE CRC64;

Query Match 80.3%; Score 469; DB 1; Length 113;
Best Local Similarity 79.5%; Pred. No. 4.8e-41;
Matches 89; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGVYLDWYLOKPGSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGVYLDWYLOKPGSPHLLIYLGSRD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 112

RESULT 7
KV2A HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; B91639; K2HUCM.
DR HSSP; P01751; INQB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 24 95 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 79.5%; Score 464.5; DB 1; Length 115;
Best Local Similarity 82.3%; Pred. No. 1.4e-40;
Matches 93; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGVYLDWYLOKPGSPHLLIYLGSNR 59
Db 2 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGVYLDWYLOKPGSPHLLIYLSYR 61

Qy 60 ASGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 112
Db 62 ASGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 114

RESULT 8
Q65ZQ7 PRELIMINARY; PRT; 248 AA.
ID Q65ZQ7
AC Q65ZQ7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON TER 248 248
SQ SEQUENCE 248 AA; 28634 MW; 7A3759B43E570950 CRC64;

Query Match 77.1%; Score 450; DB 2; Length 248;
Best Local Similarity 76.8%; Pred. No. 1.2e-38;
Matches 86; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGVYLDWYLOKPGSPHLLIYLGSNRA 60
Db 136 DVLMTQSLPLVSLGDAQSISCRSQIIVHSGNTYLEWYLOKPGSPKLLIYKSNRF 195

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 112
Db 196 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQQSPITFGQGRLEIK 247

RESULT 9
Q6P491 PRELIMINARY; PRT; 239 AA.
ID Q6P491
AC Q6P491
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN (1)_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Mullahy S.J.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez Y.S.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez Y.S., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063599; AAH63599.1; -;
 DR HSSP; P01837; IKCU.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
 Query Match 76.5%; Score 447; DB 2; Length 239;
 Best Local Similarity 76.5%; Pred. No. 2.3e-38;
 Matches 88; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
 QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLRLNGYNYLDWYKQPCQSPHLLIYLGNSRA 60
 DB 21 DIVMTQSLPLPVTGEPASISCRSSQSLRLNGYNYLDWYKQPCQSPHLLIYKISNRF 80
 QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQGTREIK 112
 DB 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQVSHFPRTFGQGTREIK 132
 RESULT 10
 Q8TCD0 PRELIMINARY; PRT; 239 AA.
 ID Q8TCD0;
 AC Q8TCD0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN (1)_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Mullahy S.J.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez Y.S., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH22362.1; -;
 DR PIR; S22658; S22658.
 DR PIR; S34095; S34095.
 DR PIR; S40324; S40324.
 DR PIR; S40374; S40374.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR HSSP; P01834; 117Z.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
 Query Match 76.4%; Score 446; DB 2; Length 239;
 Best Local Similarity 76.8%; Pred. No. 2.9e-38;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLRLNGYNYLDWYKQPCQSPHLLIYLGNSRA 60
 DB 21 DIVMTQSLPLPVTGEPASISCRSSQSLRLNGYNYLDWYKQPCQSPHLLIYKYSNRD 80
 QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQGTREIK 112
 DB 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQGTHTWPFSTFGQGTREIK 132
 RESULT 11
 KV2F HUMAN
 ID KV2F HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=86041852; PubMed=2997711;
RA Kloebeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPM1 6410.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
FT NON TER 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;
Query Match 76.08; Score 444; DB 1; Length 133;
Best Local Similarity 77.78; Pred. No. 2.3e-38;
Matches 87; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 21 DVVMTQSLPLVPTLGGQPAISICRSSLVYSDGNTYLNWFQRPQSPRLIYKYSNRD 80
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYCMQAQQSPITFGQGRLEIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYCMQGHWSWTFQGRKVEIK 132
RESULT 12
KV2G MOUSE
ID KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
```

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RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
DR PIR; A01914; KVM526.
DR HSP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;
Query Match 74.88; Score 437; DB 1; Length 113;
Best Local Similarity 75.98; Pred. No. 1e-37;
Matches 85; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DVVMTQSLPLVSLGQASISCRSSLVHSGNTYLNWYLOKAGSPRLIYKYSNRF 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYCMQAQQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGIYFCSTTHVPPTFGGKLEIK 112
RESULT 13
Q9UL80
ID Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSP; P01625; I1VE.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
FT NON TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
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Query Match 73.4%; Score 428.5; DB 2; Length 114;
Best Local Similarity 76.1%; Pred. No. 8.1e-37;
Matches 86; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEASISCRSSQSLRSGYNYLDWYKQKPGQSPHLLIYLGSNRA 60
DB 1 DVMTQSPSLPVTLRQPAISICRSPVSDGNTYLNWFQRPQSPRLLIYKVSNRD 60

QY 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQ-SPTFGQGTREIK 112
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQGTTHPPPTFGQGTREIK 113

RESULT 14
Q65ZC0 PRELIMINARY; PRT; 219 AA.

AC Q65ZC0;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t 1";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL: Z37499; CAA85724.1; --
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003196; Ig_v.
DR Pfam: PF07654; C1-set; I.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 73.3%; Score 428; DB 2; Length 219;
Best Local Similarity 75.0%; Pred. No. 2e-36;
Matches 84; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEASISCRSSQSLRSGYNYLDWYKQKPGQSPHLLIYLGSNRA 60
DB 1 ELVMTQSPSLSVLSGDAQASISCRSSQSLVHTNGNTYLNWYKQKPGSLPKLLIYVSNRF 60

QY 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSPITFGQGTREIK 112
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLVGYFCSTHVPFTFGGKLEIK 112

RESULT 15
KV2F_MOUSE STANDARD; PRT; 113 AA.

AC KV2F_MOUSE
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7534.1.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides";
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM578.
DR HSSP; O99M37; 119I.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.9%; Score 420; DB 1; Length 113;
Best Local Similarity 75.0%; Pred. No. 6.2e-36;
Matches 84; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEASISCRSSQSLRSGYNYLDWYKQKPGQSPHLLIYLGSNRA 60
DB 1 DIVMTQSPALVTGGSVSISCRSSKSLHNGNTYLNWYKQKPGQSPHLLIYRNSLA 60

QY 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGYVYCMQAQQSPITFGQGTREIK 112
DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQOREPYTFGGGKLEIK 112

Search completed: November 16, 2005, 22:01:50
Job time : 63.7941 secs

(0250) MAY 11 1964 CHIL

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 19.0441 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-2

Perfect score: 584

Sequence: 1 DIVMTQSLPLVPTGEPAS.....CMQAQSPITFGGTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	94.7	113	3	US-09-025-769B-15
2	553	94.7	113	4	US-09-490-070A-15
3	553	94.7	113	4	US-09-490-153-15
4	553	94.7	113	4	US-09-490-324-15
5	550	94.2	112	4	US-09-254-180C-9
6	536	91.8	112	1	US-08-331-398A-49
7	536	91.8	112	2	US-08-331-397B-49
8	536	91.8	112	2	US-08-759-804A-49
9	536	91.8	112	3	US-09-227-693-49
10	532	91.1	114	3	US-09-025-769B-29
11	532	91.1	114	3	US-09-025-769B-45
12	532	91.1	114	4	US-09-490-070A-29
13	532	91.1	114	4	US-09-490-070A-45
14	532	91.1	114	4	US-09-490-153-29
15	532	91.1	114	4	US-09-490-153-45
16	532	91.1	114	4	US-09-490-324-29
17	532	91.1	114	4	US-09-490-324-45
18	532	91.1	281	3	US-09-025-769B-178
19	532	91.1	281	4	US-09-490-070A-178
20	532	91.1	281	4	US-09-490-153-178
21	532	91.1	281	1	US-09-490-324-178
22	527	90.2	112	1	US-08-053-171-16
23	521	89.2	113	1	US-08-082-623-4
24	511	87.5	239	4	US-10-000-489-8
25	509	87.2	112	3	US-09-000-088-2
26	508	87.0	112	3	US-09-240-274-30
27	507	86.8	108	1	US-08-488-113B-151

Sequence 151, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 151, App
Sequence 15, Appl
Sequence 151, App
Sequence 15, App
Sequence 151, App
Sequence 151, App
Sequence 88, Appl
Sequence 88, Appl
Sequence 115, App
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-15

Query Match 94.7%; Score 553; DB 3; Length 113;
Best Local Similarity 94.6%; Pred. No. 7.3e-47;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112
Db 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112

RESULT 2

US-09-490-070A-15
; Sequence 15, Application US/09490070A
; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

FILING DATE: 24-Jan-2000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-070A-15

Query Match

Best Local Similarity 94.7%; Score 553; DB 4; Length 113;

Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60

Db 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112

Db 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112

RESULT 3

US-09-490-153-15

; Sequence 15, Application US/09490153

; Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-153-15

Query Match

Best Local Similarity 94.7%; Score 553; DB 4; Length 113;

Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60

Db 1 DIVMTQSLPLPVTGPGPASTSCRSQSLLSNGYNYLDWYLOKPGOSPILLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112

Db 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYYCMQAQOSPITFGGTRLEIK 112

RESULT 4

US-09-490-324-15

; Sequence 15, Application US/09490324

; Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries
;; NUMBER OF SEQUENCES: 373
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; FILING APPLICATION NUMBER: US/09/490,324
;; FILING DATE: 24-Jan-2000

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090

;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>

;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-324-15

Query Match 94.7%; Score 553; DB 4; Length 113;
Best Local Similarity 94.6%; Pred. No. 7.3e-47;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

RESULT 5

US-09-254-180C-9
;; Sequence 9, Application US/09254180C
;; Patent No. 6777540

;; GENERAL INFORMATION:

;; APPLICANT: OKUMURA, Ko

;; APPLICANT: EDA, Yasuyuki

;; APPLICANT: MAEDA, Hiroaki

;; APPLICANT: USHIO, Yoshitaka

;; APPLICANT: HIGUCHI, Hirofumi

;; APPLICANT: NAKATA, Motoni

;; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
;; INFORMATION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand

;; FILE REFERENCE: 050006-0055

;; CURRENT APPLICATION NUMBER: US/09/254,180C

;; CURRENT FILING DATE: 1999-04-15

;; PRIOR APPLICATION NUMBER: PCT/JP97/02983

;; PRIOR FILING DATE: 1997-08-27

;; PRIOR APPLICATION NUMBER: 271546/1996

;; PRIOR FILING DATE: 1996-09-20

;; PRIOR APPLICATION NUMBER: 231472/1996

;; PRIOR FILING DATE: 1996-09-02
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-254-180C-9

Query Match 94.2%; Score 550; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.4e-46;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

RESULT 6

US-08-331-398A-49
;; Sequence 49, Application US/08331398A
;; Patent No. 5608039

;; GENERAL INFORMATION:

;; APPLICANT: Paetan, Ira

;; APPLICANT: Willingham, Mark

;; APPLICANT: Fitzgerald, David

;; APPLICANT: Brinkmann, Ulrich

;; APPLICANT: Pai, Lee

;; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
;; and Their Uses (as amended)

;; NUMBER OF SEQUENCES: 68

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew

;; STREET: One Market Plaza, Steuart Street Plaza

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94105-1492

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA: US/08/331,398A

;; APPLICATION NUMBER: US/08/331,398A

;; FILING DATE: 28-OCT-1994

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/767,331

;; FILING DATE: 30-SEP-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/596,289

;; FILING DATE: 12-OCT-1990

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hunter, Tom

;; REGISTRATION NUMBER: 38,498

;; REFERENCE/DOCKET NUMBER: 015280-126110US

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 543-9600

;; TELEFAX: (415) 543-5043

;; INFORMATION FOR SEQ ID NO: 49:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 112 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; FEATURE:

;; NAME/KEY: Protein

Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 9
US-09-227-693-49
; Sequence 49, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ita
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-136-1-3
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"

US-09-227-693-49
Query Match 91.8%; Score 536; DB 3; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.3e-45;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 10
US-09-025-769B-29
; Sequence 29, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-025-769B-29
Query Match 91.1%; Score 532; DB 3; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLVPTGPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 11
US-09-025-769B-45
; Sequence 45, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 45:
LENGTH: 114 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
US-09-025-769B-45

Query Match 91.1%; Score 532; DB 3; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPVTGEPASISCRSSQSLLRSNGYNLYDWLYQKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLVPVTGEPASISCRSSQSLLRSNGYNLYDWLYQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQQSPITFGQGRLEIK 112
Db 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQQSPITFGQGRLEIK 112

RESULT 12
US-09-490-070A-29
Sequence 29, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-29

Query Match 91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Db 1 DIVMTQSLPLVPVTGEPASISCRSSQSLLRSNGYNLYDWLYQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQQSPITFGQGRLEIK 112
Db 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQQSPITFGQGRLEIK 112

RESULT 13
US-09-490-070A-45
Sequence 45, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRIK 112

RESULT 14
US-09-490-153-29
; Sequence 29, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASPISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
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Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRIK 112

RESULT 15
US-09-490-153-45
; Sequence 45, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-153-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-153-29

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRIK 112

RESULT 15
US-09-490-153-45
; Sequence 45, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-153-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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Qy	1	DIVMTQSP	LSLPVT	PGEPAS	ISCRSS	QSLLRS	NGYN	LDWY	LQKPG	QSPHLL	IYLG	SNRA	60
Db	1	DIVMTQSP	LSLPVT	PGEPAS	ISCRSS	QSLLRS	NGYN	LDWY	LQKPG	QSPHLL	IYLG	SNRA	60
Qy	61	SGVDPDR	FSGSG	GTDF	TLKISR	VEAD	VGYY	CMQA	QSPIT	FCQGT	RLEIK	112	
Db	61	SGVDPDR	FSGSG	GTDF	TLKISR	VEAD	VGYY	CMQA	QSPIT	FCQGT	RLEIK	112	

Search completed: November 16, 2005, 22:07:17
Job time : 19.0441 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 68.7647 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-2
Perfect score: 584
Sequence: 1 DIWVTQSLPLVTPGPAS.....CMQAQSPITFGQGTRLRIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
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 - 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
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 - 22: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	584	100.0	112	14	US-10-330-530-2
3	584	100.0	112	16	US-10-660-357-2
4	556	95.2	112	20	US-11-021-715-93
5	554	94.9	112	15	US-10-292-088-52
6	554	94.9	239	15	US-10-292-088-56
7	553	94.7	112	15	US-10-292-088-104
8	553	94.7	112	20	US-11-021-715-75
9	553	94.7	112	20	US-11-021-715-90
10	552	94.5	112	20	US-11-021-715-74
11	552	94.5	112	20	US-11-021-715-86
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 93, Appli					
Sequence 52, Appli					
Sequence 56, Appli					
Sequence 104, Appli					
Sequence 75, Appli					
Sequence 90, Appli					
Sequence 74, Appli					
Sequence 86, Appli					

12	552	94.5	134	17	US-10-858-855-8	Sequence 8, Appli
13	551	94.3	112	20	US-11-021-715-87	Sequence 87, Appli
14	549.5	94.1	113	20	US-11-021-715-89	Sequence 89, Appli
15	548	93.8	112	15	US-10-292-088-103	Sequence 103, Appli
16	548	93.8	112	15	US-10-292-088-111	Sequence 111, Appli
17	548	93.8	112	17	US-10-877-773-30	Sequence 30, Appli
18	548	93.8	112	17	US-10-877-774-30	Sequence 30, Appli
19	548	93.8	112	17	US-10-735-916A-58	Sequence 58, Appli
20	548	93.8	112	20	US-11-021-715-91	Sequence 91, Appli
21	548	93.8	113	15	US-10-308-817-177	Sequence 177, Appli
22	548	93.8	113	15	US-10-453-698-177	Sequence 177, Appli
23	548	93.8	113	17	US-10-726-332-212	Sequence 212, Appli
24	548	93.8	125	14	US-10-010-942B-6	Sequence 6, Appli
25	548	93.8	125	15	US-10-388-389-6	Sequence 6, Appli
26	548	93.8	125	16	US-10-703-713-6	Sequence 6, Appli
27	548	93.8	125	16	US-10-704-070-6	Sequence 6, Appli
28	548	93.8	125	17	US-10-232-030-6	Sequence 18, Appli
29	546	93.5	112	14	US-10-269-805-18	Sequence 26, Appli
30	546	93.5	112	14	US-10-269-805-26	Sequence 26, Appli
31	546	93.5	112	15	US-10-309-762-33	Sequence 33, Appli
32	545.5	93.4	113	20	US-11-021-715-88	Sequence 63, Appli
33	545	93.3	112	16	US-10-663-244-63	Sequence 77, Appli
34	545	93.3	112	20	US-11-021-715-77	Sequence 81, Appli
35	545	93.3	112	20	US-11-021-715-81	Sequence 92, Appli
36	545	93.3	112	20	US-11-021-715-92	Sequence 145, Appli
37	545	93.3	238	16	US-10-663-244-145	Sequence 123, Appli
38	544.5	93.2	112	20	US-11-031-485-123	Sequence 4, Appli
39	544.5	93.2	238	20	US-11-031-485-4	Sequence 82, Appli
40	544	93.2	112	20	US-11-021-715-82	Sequence 215, Appli
41	543.5	93.1	112	17	US-10-726-332-215	Sequence 12, Appli
42	542	92.8	112	15	US-10-292-088-12	Sequence 28, Appli
43	542	92.8	112	15	US-10-292-088-28	Sequence 60, Appli
44	542	92.8	112	15	US-10-292-088-60	Sequence 94, Appli
45	542	92.8	112	15	US-10-292-088-94	

ALIGNMENTS

RESULT 1
US-10-330-613-2
; Sequence 2, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-2

Query Match	100.0%;	Score 584;	DB 14;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 7.3e-46;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	SGVPDRFSGSGGTFTLTKISRVAEDVGYVCWQAQSPITFGQGTRLRIK	112	
Db	61	SGVPDRFSGSGGTFTLTKISRVAEDVGYVCWQAQSPITFGQGTRLRIK	112	

RESULT 2

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US-10-330-530-2
; Sequence 2, Application US/10330530
; Publication No. US2003015251A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-2
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Best Local Similarity 100.0%; Pred. No. 7.3e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 112
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RESULT 3
US-10-660-357-2
; Sequence 2, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menache
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-2
Query Match 100.0%; Score 584; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.3e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 112
Db 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 112

RESULT 4
US-11-021-715-93
; Sequence 93, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: AUTOANTIBODIES AND INHIBITORS THEREOF
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-93
Query Match 95.2%; Score 556; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.7e-43;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 111
Db 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 111

RESULT 5
US-10-292-088-52
; Sequence 52, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-52
Query Match 94.9%; Score 554; DB 15; Length 112;
Best Local Similarity 94.6%; Pred. No. 4.1e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPEPASISCRSSQSLRLSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60

Qy 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 112
Db 61 SGVDPFRSGSGGTDFTLKISRVEAEDGVMYVYCMQAQOSPITFGQGTGLEIK 112

RESULT 6
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
```



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; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-088-56

Query Match          94.7%; Score 554; DB 15; Length 239;
Best Local Similarity 94.6%; Pred. No. 9.1e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 21 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 132

RESULT 7
US-10-292-088-104
; Sequence 104, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-088-104

Query Match          94.7%; Score 553; DB 15; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112

RESULT 8
US-11-021-715-75
; Sequence 75, Application US/11021715

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; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-021-715-75

Query Match          94.7%; Score 553; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112

RESULT 9
US-11-021-715-90
; Sequence 90, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-021-715-90

Query Match          94.7%; Score 553; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSHRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112

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RESULT 10
US-11-021-715-74
; Sequence 74, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-74

Query Match          94.5%; Score 552; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 6.2e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112

RESULT 11
US-11-021-715-86
; Sequence 86, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-86

Query Match          94.5%; Score 552; DB 20; Length 112;
Best Local Similarity 95.5%; Pred. No. 6.2e-43;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112
```

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Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112

RESULT 12
US-10-858-855-8
; Sequence 8, Application US/10858855
; Publication No. US20050118651A1
; GENERAL INFORMATION:
; APPLICANT: BASI, Guriq
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; TITLE OF INVENTION: AMYLOID PEPTIDE
; FILE REFERENCE: ELN-028
; CURRENT APPLICATION NUMBER: US/10/858,855
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: 60/474654
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-858-855-8

Query Match          94.5%; Score 552; DB 17; Length 134;
Best Local Similarity 93.8%; Pred. No. 7.5e-43;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 23 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPQLLIYLGSNRA 82
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112
Db 83 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 134

RESULT 13
US-11-021-715-87
; Sequence 87, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-87

Query Match          94.3%; Score 551; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 7.7e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
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Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 112

RESULT 14

US-11-021-715-89
; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021.715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match 94.1%; Score 549.5; DB 20; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.1e-42;
Matches 107; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGYNVLDWYLOKPGOSPQLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGYNVLDWYLOKPGOSPQLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 113

RESULT 15

US-10-292-088-103
; Sequence 103, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292.088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-103

Query Match 93.8%; Score 548; DB 15; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGYNVLDWYLOKPGOSPQLLIYLGSNRA 60

Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGYNVLDWYLOKPGOSPQLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQTRLEIK 112

Search completed: November 16, 2005, 23:05:39
Job time : 69.7647 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: us-10-660-357A-6

Perfect score: 555

Sequence: 1 EIWQTSPATLSVSGERAT.....COQYNNWPRTFQGTGKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A: Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	7	Adc99777 Anti-huma
2	555	100.0	107	7	Add05381 Anti-MUC1
3	555	100.0	107	7	Adf09819 Human ant
4	546	98.4	107	7	Adc99805 Anti-huma
5	546	98.4	107	7	Adc99805 Anti-MUC1
6	546	98.4	107	7	Add05409 Anti-MUC1
7	546	98.4	107	7	Add05442 Anti-MUC1
8	546	98.4	107	7	Adf09847 Human ant
9	536	97.1	107	6	Adf09847 Light cha
10	536	96.6	107	6	Adf09847 Light cha
11	536	96.6	107	6	Adf09847 Light cha
12	536	96.6	107	8	Adp22404 Human ant
13	536	96.6	107	8	Adp22407 Human ant
14	536	96.6	107	8	Adp22407 Human ant
15	536	96.6	107	8	Adp22407 Human ant
16	534	96.2	107	6	Adf09847 Light cha
17	533	96.1	108	6	Adf09847 Light cha
18	533	96.0	107	6	Adf09847 Light cha
19	533	96.0	107	8	Adp22408 Human ant
20	532	95.9	250	5	Adp22408 Human ant
21	532	95.9	250	7	Adp22408 Human ant
22	529	95.4	117	3	Adf09847 Light cha
23	529	95.4	117	6	Adf09847 Light cha
24	529	95.4	117	6	Adf09847 Light cha
25	529	95.4	117	6	Adf09847 Light cha

26	529.5	95.4	117	6	ABR42857	Abw02466 Human mon
27	529.5	95.4	117	7	ABW02446	Abw02466 Human mon
28	529.5	95.4	117	7	ABW02466	Abw02466 Human mon
29	529.5	95.4	117	7	ABW02465	Abw02465 Human mon
30	529	95.3	246	5	ABP45257	Abp45257 Human Bly
31	529	95.3	246	7	ADG96084	Adg96084 Single ch
32	528	95.1	107	6	ABR54889	Abf54889 Light cha
33	526	94.8	107	7	ADJ80364	Adj80364 Human ant
34	525	94.6	107	8	ADP22278	Adp22278 Human ant
35	525	94.6	107	8	ADP22278	Adp22278 Human ant
36	525	94.6	127	7	ADG61110	Adg61110 Human ant
37	524	94.5	106	8	ADP22371	Adp22371 Human ant
38	524	94.4	154	8	ADL25472	Adl25472 Human mab
39	522.5	94.1	117	6	ABR42850	Abf42850 Tumour-sp
40	522.5	94.1	117	6	ABR42851	Abf42851 Tumour-sp
41	522.5	94.1	117	6	ABR42849	Abf42849 Tumour-sp
42	522.5	94.1	117	6	ABR42853	Abf42853 Tumour-sp
43	522.5	94.1	117	7	ABW02460	Abw02460 Human mon
44	522.5	94.1	117	7	ABW02462	Abw02462 Human mon
45	522.5	94.1	117	7	ABW02459	Abw02459 Human mon

ALIGNMENTS

RESULT 1

ADC99777

ID ADC99777 standard; protein; 107 AA.

XX

AC ADC99777;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

OS Homo sapiens.

XX

XX WO2003057838-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

PA (ABGE-) ABGENIX INC.

 XX || PI | Gudas J; |
XX	
XX	WPI; 2003-587113/55.
DR	N-P8DB; ADC99779.
XX	
XX	New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT	or condition associated with expression of MUC18 in a patient, e.g.
PT	tumors, cancers, and other malignancies.
XX	
PS	Claim 3; SEQ ID NO 6; 78pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody comprising
CC	a heavy or light chain amino acid or a heavy or light chain variable
CC	domain where the antibody binds to MUC18. The monoclonal antibody of the
CC	invention demonstrates cytostatic activity and may be useful for treating
CC	a disease or condition associated with the expression of MUC18 on the
CC	cell surface such as tumours, specifically melanoma, oesophageal,
CC	pancreatic or colorectal tumours, carcinomas, particularly cervical
CC	carcinomas and cervical intraepithelial neoplasia and cancers including
CC	colorectal, breast or lung cancer, as well as other malignancies. The
CC	current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 4e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 2

ADD05381

ID ADD05381 standard; protein; 107 AA.

XX AC ADD05381;

DT 01-JAN-2004 (first entry)

XX Anti-MUC18 antibody light chain variable region protein, SEQ ID No 6.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX OS Homo sapiens.

XX PN WO2003057006-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041582.

XX PR 28-DEC-2001; 2001US-0346460P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Bar-Eli M;

XX DR WPI; 2003-577496/54.

XX DR N-PSDB; ADD05383.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

XX treating tumors, inhibiting tumor growth, inhibiting cell invasion

XX associated with melanoma, or increasing survival of an animal having a

XX metastatic tumor.

XX Claim 3; SEQ ID NO 6; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting

XX tumor growth in an animal. The tumor inhibition process comprises

XX selecting an animal in need of treatment for a tumor, providing a

XX monoclonal antibody comprising a heavy chain amino acid, where the

XX antibody consists of any one of 10 fully defined sequences of 117-123

XX amino acids given in the specification, and where the monoclonal antibody

XX binds MUC18, and contacting the tumor with the antibody resulting in

XX inhibited proliferation of the cells. The monoclonal antibody has

XX cytostatic and can be used in the production of a vaccine. The monoclonal

XX antibodies against the MUC18 antigen are useful for diagnosing and

XX treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumour or

XX tumour metastasis), inhibiting cell invasion associated with melanoma, or

XX increasing survival of an animal having a metastatic tumour. This

XX sequence represents an anti-MUC18 antibody light chain, variable region,

XX protein of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 4e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

Best Local Similarity 100.0%; Pred. No. 4e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 3

ADF09819

ID ADF09819 standard; protein; 107 AA.

XX AC ADF09819;

DT 12-FEB-2004 (first entry)

XX Human anti-MUC18 monoclonal antibody light chain #2.

XX cell proliferation inhibition; MUC18 tumour antigen;

XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

XX carcinoma; cancer; malignancy; light chain; human.

XX OS Homo sapiens.

XX PN WO2003057837-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041580.

XX PR 28-DEC-2001; 2001US-0346414P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-598367/56.

XX DR N-PSDB; ADF09821.

XX Inhibiting cell proliferation associated with expression of MUC18 tumour

XX antigen, involves incubating and inhibiting cell by administering anti-

XX MUC18 monoclonal antibody.

XX Claim 3; SEQ ID NO 6; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation

XX associated with expression of MUC18 tumour antigen. The method involves

XX administering anti-MUC18 monoclonal antibody. The method of the invention

XX is useful for inhibiting cell (e.g. melanoma or tumour cell)

XX proliferation associated with the expression of MUC18 tumour antigen, the

XX method is preferably useful for inhibiting tumour metastasis. The method

XX is useful for inhibiting cell proliferation in patients with tumours,

XX carcinomas, cancer and other malignancies. The present amino acid

XX sequence represents a light chain from an MUC18 tumour antigen-specific

XX monoclonal antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 4e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 4
 ADC99805
 ID ADC99805 standard; protein; 107 AA.
 AC ADC99805;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34.
 XX
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytototoxic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057838-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041581.
 XX
 PR 28-DEC-2001; 2001US-0346299P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J;
 XX
 DR WPI; 2003-587113/55.
 DR N-PSDB; ADC99807.
 XX
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.
 PT
 XX
 PS Claim 3; SEQ ID NO 34; 78pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC light chain protein of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 98.4%; Score 546; DB 7; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.9e-33;
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFQGQTKVEIK 107
 DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFQGQTKVEIK 107
 RESULT 5
 ADD05409
 ID ADD05409 standard; protein; 107 AA.
 XX
 AC ADD05409;
 XX

DT 01-JAN-2004 (first entry)
 XX
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 34.
 XX
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057006-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041582.
 XX
 PR 28-DEC-2001; 2001US-0346460P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J, Bar-Eli M;
 XX
 DR WPI; 2003-577496/54.
 DR N-PSDB; ADD05411.
 XX
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.
 PT
 XX
 PS Claim 3; SEQ ID NO 34; 87pp; English.
 XX
 CC The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123
 CC amino acids given in the specification, and where the monoclonal antibody
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC sequence represents an anti-MUC18 antibody light chain, variable region,
 CC protein of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 98.4%; Score 546; DB 7; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.9e-33;
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFQGQTKVEIK 107
 DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFQGQTKVEIK 107
 RESULT 6
 ADD05442
 ID ADD05442 standard; protein; 107 AA.
 XX
 AC ADD05442;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID 67.
 XX
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

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KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX Unidentified.
OS
XX WO2003057006-A2.
PN
XX 17-JUL-2003.
PD
XX 26-DEC-2002; 2002WO-US041582.
PF
XX 28-DEC-2001; 2001US-0346460P.
PR
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J, Bar-Eli M;
PI WPI; 2003-577496/54.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX Disclosure; SEQ ID NO 67; 87pp; English.
PS
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
XX Sequence 107 AA;
SQ
Query Match 98.4%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.9e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
RESULT 7
ADF09847
ID ADF09847 standard; protein; 107 AA.
AC
XX ADF09847;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human anti-MUC18 monoclonal antibody light chain #9.
DE
XX cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
XX Homo sapiens.
OS
XX WO2003057837-A2.
PN
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX Unidentified.
OS
XX WO2003057006-A2.
PN
XX 17-JUL-2003.
PD
XX 26-DEC-2002; 2002WO-US041580.
PF
XX 28-DEC-2001; 2001US-0346414P.
PR
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J;
PI WPI; 2003-598367/56.
XX N-PSDB; ADF09849.
DR
XX Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
XX Claim 3; SEQ ID NO 34; 83pp; English.
PS
XX The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
XX Sequence 107 AA;
SQ
Query Match 98.4%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.9e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
RESULT 8
ABR54896
ID ABR54896 standard; protein; 107 AA.
XX
XX ABR54896;
XX
XX 30-JUN-2003 (first entry)
DT
XX Light chain clone HBPAXK2d 3A9 SEQ ID NO:122.
DE
XX Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO2003025202-A2.
PN
XX 27-MAR-2003.
PD
XX 13-SEP-2002; 2002WO-US029889.
PF
XX 19-SEP-2001; 2001US-0323455P.
PR
XX (ALEX-) ALEXION PHARM INC.
PA
XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
PI
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XX DR WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PT sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107 AA;
XX
XX Query Match 97.8%; Score 543; DB 6; Length 107;
XX Best Local Similarity 98.1%; Pred. No. 3.1e-33;
XX Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
DB |||||
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNWPTFGQTKVEIK 107
DB |||||
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNWPTFGQTKVEIK 107

RESULT 9
ABR54900
ID ABR54900 standard; protein; 107 AA.
XX AC ABR54900;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3D12 SEQ ID NO:126.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX

PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PT sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107 AA;
XX
XX Query Match 97.1%; Score 539; DB 6; Length 107;
XX Best Local Similarity 97.2%; Pred. No. 6.2e-33;
XX Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
DB |||||
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNWPTFGQTKVEIK 107
DB |||||
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNWPTFGQTKVEIK 107

RESULT 10
ABR54897
ID ABR54897 standard; protein; 107 AA.
XX AC ABR54897;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3A12 SEQ ID NO:123.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX

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XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
 XX WPI; 2003-313359/30.
 XX
 XX Amplifying nucleic acid by contacting engineered nucleic acid strand
 PT having predetermined sequence at one end and sequence complementary to
 PT predetermined sequence at other end, with primer having predetermined
 PT sequence.
 XX
 PS Example 3; Fig 8b-c; 68pp; English.
 XX
 CC The present invention describes a method (M1) for amplifying a nucleic
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other, and contacting (S) with a
 CC primer having the predetermined sequence in the presence of a polymers
 CC and nucleotides under conditions suitable for polymerisation of the
 CC nucleotides. Also described is an engineered nucleic acid strand (I)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other end. M1 is useful for
 CC amplifying a nucleic acid. M1 can be used for producing an antibody
 CC library. M1 is useful for preparing amplified products that can be
 CC ligated into a suitable expression vector, where the vector can be used
 CC to transform an appropriate host organism to produce the polypeptide or
 CC protein encoded by the target sequence. M1 is useful to amplify a family
 CC of related sequences to build a complex library such as, for example an
 CC antibody library. M1 is useful not only for producing large amounts of
 CC one target nucleic acid sequence, but also for amplifying simultaneously
 CC more than one different target nucleic acid sequence located on the same
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
 CC ABR54998 represent sequence used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 107 AA;
 Query Match 96.6%; Score 536; DB 6; Length 107;
 Best Local Similarity 96.3%; Pred. No. 1e-32;
 Matches 103; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRSQSQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 Db 1 EIVMTQSPATLSVSPGERATLSCRSQSQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTGKVEIK 107
 Db 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTGKVDIK 107
 RESULT 11
 ABR54883
 ID ABR54883 standard; protein; 107 AA.
 XX
 AC ABR54883;
 XX
 DT 30-JUN-2003 (first entry)
 XX
 DE Light chain clone HBPAX1b 3A2 SEQ ID NO:109.
 XX
 KW Engineered template; single primer amplification; antibody library;
 KW nucleic acid amplification.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2003025202-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 19-SEP-2002; 2002WO-US029889.
 PF
 XX 19-SEP-2001; 2001US-0323455P.
 PR
 XX

PA (ALEX-) ALEXION PHARM INC.
 XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
 XX WPI; 2003-313359/30.
 DR
 XX Amplifying nucleic acid by contacting engineered nucleic acid strand
 PT having predetermined sequence at one end and sequence complementary to
 PT predetermined sequence at other end, with primer having predetermined
 PT sequence.
 XX
 PS Example 3; Fig 8b-c; 68pp; English.
 XX
 CC The present invention describes a method (M1) for amplifying a nucleic
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other, and contacting (S) with a
 CC primer having the predetermined sequence in the presence of a polymers
 CC and nucleotides under conditions suitable for polymerisation of the
 CC nucleotides. Also described is an engineered nucleic acid strand (I)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other end. M1 is useful for
 CC amplifying a nucleic acid. M1 can be used for producing an antibody
 CC library. M1 is useful for preparing amplified products that can be
 CC ligated into a suitable expression vector, where the vector can be used
 CC to transform an appropriate host organism to produce the polypeptide or
 CC protein encoded by the target sequence. M1 is useful to amplify a family
 CC of related sequences to build a complex library such as, for example an
 CC antibody library. M1 is useful not only for producing large amounts of
 CC one target nucleic acid sequence, but also for amplifying simultaneously
 CC more than one different target nucleic acid sequence located on the same
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
 CC ABR54998 represent sequence used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 107 AA;
 Query Match 96.6%; Score 536; DB 6; Length 107;
 Best Local Similarity 96.3%; Pred. No. 1e-32;
 Matches 103; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRSQSQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 Db 1 EIVMTQSPATLSVSPGERATLSCRSQSQSVNNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTGKVEIK 107
 Db 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTGKRLK 107
 RESULT 12
 ADP22404
 ID ADP22404 standard; protein; 107 AA.
 XX
 AC ADP22404;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFA antibody light chain variable region SEQ ID NO:310.
 XX
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX

OS Homo sapiens.
PN WO2004050683-A2.
XX 17-JUN-2004.
XX 02-DEC-2003; 2003WO-US038281.
XX 02-DEC-2002; 2002US-0430729P.
XX (ABGE-) ABGENIX INC.
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX WPI; 2004-480601/45.
XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 310; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC the sample; (2) a composition comprising the antibody and TNFa in
CC the sample; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody light chain variable region, which is used in the
XX exemplification of the present invention.
SQ Sequence 107 AA;
Query Match 96.6%; Score 536; DB 8; Length 107;
Best Local Similarity 96.3%; Pred. No. 1e-32;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTSPATLSVSGERATLSCRSQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTSPATLSVSGERATLSCRSQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGTKVEIK 107
RESULT 13
ADP22407

ID ADP22407 standard; protein; 107 AA.
XX AC ADP22407;
XX DT 09-SEP-2004 (first entry)
XX DE Human anti-TNFA antibody light chain variable region SEQ ID NO:313.
XX KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoaric; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX OS Homo sapiens.
XX PN WO2004050683-A2.
XX 17-JUN-2004.
XX 02-DEC-2003; 2003WO-US038281.
XX 02-DEC-2002; 2002US-0430729P.
XX (ABGE-) ABGENIX INC.
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX WPI; 2004-480601/45.
XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX Example 10; SEQ ID NO 313; 213pp; English.
XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC the sample; (2) a composition comprising the antibody and TNFa in
CC the sample; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody light chain variable region, which is used in the
XX exemplification of the present invention.

CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-32;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 14
ADRA43402
ID ADRA43402 standard; protein; 107 AA.

XX AC ADRA43402;

XX DT 04-NOV-2004 (first entry)

XX DE Human anti-IgE antibody light chain L16 and JK4.

XX KW antibody; variable light chain; variable heavy chain; Antiallergic;
XX Dermatological; Immunosuppressive; IGE; asthma; allergic rhinitis;
XX eczema; urticaria; atopic dermatitis; food allergy; CDR.

XX OS Homo sapiens.

XX PN WO2004070011-A2.

XX PD 19-AUG-2004.

XX PF 02-FEB-2004; 2004WO-US002894.

XX PR 01-FEB-2003; 2003US-0444229P.

XX PA (TANO-) TANOX INC.

XX PI Singh S, Foster C, Wu H;

XX PS WPI; 2004-604433/58.

XX PT New high affinity human monoclonal antibodies, particularly those
PT directed against isotypic determinants of immunoglobulin E, useful for
PT asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a
PT food allergy.

XX PS Disclosure; SEQ ID NO 2; 101pp; English.

XX CC The present invention relates to an antibody comprising a variable light
CC chain region or a variable heavy chain region. The antibody and methods
CC are useful for treating a disorder associated with an abnormally high IgE
CC level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic
CC dermatitis, or a food allergy. The present sequence represents human anti
CC -IgE antibody light chain combined L16 and JK4.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-32;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 15
ADR31547

ID ADR31547 standard; protein; 107 AA.

XX AC ADR31547;

XX DT 04-NOV-2004 (first entry)

XX DE L16/JK4 human light chain consensus sequence template.

XX KW Antibody; diagnostic; prophylaxis; therapy; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX Region 24..34
FT /note= "Kabat CDR"
FT Region 50..56
FT /note= "Kabat CDR"
FT Region 89..97
FT /note= "Kabat CDR"

XX PN WO2004070010-A2.

XX PD 19-AUG-2004.

XX PF 02-FEB-2004; 2004WO-US002892.

XX PR 01-FEB-2003; 2003US-0444229P.

XX PA (TANO-) TANOX INC.

XX PI Singh S, Foster C, Wu H;

XX PS WPI; 2004-604432/58.

XX PT Generating a humanized, high affinity antibody from an antibody of
XX interest comprises selecting a suitable human template as the framework
XX for the H and L chain variable domains of the high affinity antibody to
XX be made.

XX PS Example 1; SEQ ID NO 2; 100pp; English.

XX CC The invention relates to a method for generating a humanised high
XX affinity antibody from an antibody of interest. The method involves
XX selecting a suitable human template as the framework for the H (heavy)
XX and L (light) chain variable (V) domains of the high affinity antibody to
XX be made. The method is useful for generating high affinity antibodies
XX useful in diagnostics, prophylaxis and treatment of diseases. The present
XX sequence is L16/JK4 human light chain consensus sequence template. This
XX sequence is used in the exemplification of the invention.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-32;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

Search completed: November 16, 2005, 21:51:36

Job time : 62.3676 secs

CHINA 2017-2024

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-6
Perfect score: 555
Sequence: 1 EIVMTQSPATLSVSPGERAT.....CQQYNWPRFTGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544	98.0	107	S34005	Ig kappa chain V r
2	536	96.6	117	S40362	Ig kappa chain - h
3	531	95.7	128	S40343	Ig kappa chain V-J
4	508.5	91.6	109	K3HUPM	Ig kappa chain V-I
5	499.5	90.0	131	S40328	Ig kappa chain - h
6	495	89.2	128	A56701	Ig kappa chain V r
7	493.5	88.9	116	B26555	Ig kappa chain V-I
8	491	88.5	111	S23628	Ig kappa chain V r
9	490.5	88.4	215	JE0244	Ig kappa chain NIG
10	484	87.2	115	K3HUCI	Ig kappa chain pre
11	483	87.0	115	A30553	Ig kappa chain pre
12	482	86.8	144	PL0106	Ig kappa chain pre
13	481	86.7	215	JE0243	Ig kappa chain NIG
14	473.5	85.3	109	D30601	Ig kappa chain V-I
15	473	85.2	95	PH0868	Ig kappa chain V r
16	473	85.2	98	I30608	Ig kappa chain V-I
17	472.5	85.1	114	S54905	Ig kappa chain V r
18	472.5	85.1	129	K3HUHA	Ig kappa chain pre
19	471	84.9	110	S40326	Ig kappa chain V-J
20	471	84.9	123	S40378	Ig kappa chain - h
21	471	84.9	128	S40379	Ig kappa chain V-J
22	470.5	84.8	109	F30607	Ig kappa chain V-I
23	468	84.3	91	S37527	Ig kappa chain V r
24	468	84.3	108	G44151	Ig kappa chain V r
25	467.5	84.2	109	K3HUSI	Ig kappa chain V-I
26	467.5	84.2	109	D30601	Ig kappa chain V-I
27	466.5	84.1	109	B30601	Ig kappa chain V-I
28	466.5	84.1	128	S20636	Ig kappa chain V r
29	465.5	83.9	129	A32274	Ig kappa chain pre

RESULT 1

S34005
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34005; S30524
R:Mariette, X.; Tsapis, A.; Brouet, J.C.
R:J. Immunol 23, 846-851, 1993.
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MAR>
A:Cross-references: EMBL:X18330
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 544; DB 2; Length 107;
Best Local Similarity 98.1%; Pred. No. 3.4e-39;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYCASTRATGIPA	60
DB	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYCASTRATGIPA	60
QY	61	RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNWPRFTGGTKVEIK	107
DB	61	RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNWPRFTGGTKVEIK	107

RESULT 2

S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40362
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 96.6%; Score 536; DB 2; Length 117;

Best Local Similarity 97.2%; Pred. No. 1.7e-38; Mismatches 1; Indels 0; Gaps 0;
Matches 104; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 60

Db 11 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 70

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107

Db 71 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 117

RESULT 3

S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 531; DB 2; Length 128;

Best Local Similarity 95.3%; Pred. No. 5e-38; Mismatches 3; Indels 0; Gaps 0;
Matches 102; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 60

Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107

Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127

RESULT 4

K3HUPM
Ig kappa chain V-III region (Pom) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01897
R:Klapper, D.G.; Capra, J.D.
Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976
A:Title: The amino acid sequence of the variable regions of the light chains from two id
A:Reference number: A01897
A:Molecule type: protein
A:Residues: 1-109 <KLA>
C:Cross-references: UNIPROT:P01624
C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;23-89/Disulfide bonds: #status predicted

Query Match 91.6%; Score 508.5; DB 1; Length 109;

Best Local Similarity 91.7%; Pred. No. 3.4e-36; Mismatches 4; Indels 1; Gaps 1;
Matches 99; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIP 59

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIP 60

QY 60 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107

Db 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 108

RESULT 5

S40328
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40328
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CAA51106.1; PID:g441345
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 499.5; DB 2; Length 131;

Best Local Similarity 89.8%; Pred. No. 2.3e-35; Mismatches 4; Indels 1; Gaps 1;
Matches 97; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 60

Db 20 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 79

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107

Db 80 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127

RESULT 6

A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are near
A:Reference number: A56701; MUID:95279371; PMID:7759488
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: GB:I41174; NID:g762823; PIDN:AAA64877.1; PID:g762824
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 495; DB 2; Length 128;

Best Local Similarity 88.8%; Pred. No. 5.3e-35; Mismatches 7; Indels 0; Gaps 0;
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 60

Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAQYQKPGQAPRLLIYGASTRATGIPA 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107

Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127


```
RESULT 7
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Widdaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an IGH monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      88.9%; Score 493.5; DB 2; Length 116;
Best Local Similarity 88.9%; Pred. No. 6.5e-35;
Matches 96; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 DIVMTQVPTLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYAASRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP-TEGQGTKEIK 107
Db 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWPITFGQGTLEIK 108

RESULT 8
S23628
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S23628
J:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
R. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740865
A:Accession: S23628
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <OLE>
A:Cross-references: EMBL:X59705; NID:G34022; PIDN:CAA42226.1; PID:gl335190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      88.5%; Score 491; DB 2; Length 111;
Best Local Similarity 88.8%; Pred. No. 1e-34;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWPTEGQGTKEIK 107
Db 61 RFGSGSGTDFLTITISLSEDFAVYVCOQRNSNPWPTFGQGTKEIK 107

RESULT 9
JE0244
Ig kappa chain IIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JFID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
```

```
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      88.4%; Score 490.5; DB 2; Length 215;
Best Local Similarity 88.9%; Pred. No. 2.1e-34;
Matches 96; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EVVLTQSPATLSVSPGERATLSCRASQSVSHNLAWYQOKPGQAPRLIIYTRASTRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNW-PRTEGQGTKEIK 107
Db 61 RFGSGSGTDFLTITISLQSEDFALYVCOQYNTWPLTFGGGTKEIK 108

RESULT 10
K3HUCL
Ig kappa chain precursor V-III region (CLL) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01898
R:Jirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A:Title: Cloning and sequence determination of a human rheumatoid factor light-chain gene
A:Reference number: A01898; MUID:86177570; PMID:3083417
A:Accession: A01898
A:Molecule type: DNA
A:Residues: 1-115 <JIR>
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:I36266
A:Map position: 2p12-2p11
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted
F:21-43/Region: framework 1
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3
F:43-108/Disulfide bonds: #status predicted

Query Match      87.2%; Score 484; DB 1; Length 115;
Best Local Similarity 97.9%; Pred. No. 4.1e-34;
Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 21 EVVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 80

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP 95
Db 81 RFGSGSGTFTLTITISLQSEDFAVYVCOQYNNWP 115

RESULT 11
A30553
Ig kappa chain precursor V-III region (Hah) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30553
```

R;Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.
J. Immunol. 142, 688-694, 1989
A;Title: Characterization of four homologous L chain variable region genes that are rela
A;Reference number: A30553; MUID:89093959; PMID:2492051
A;Accession: A30553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <LU>
A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 483; DB 2; Length 115;
Best Local Similarity 97.9%; Pred. No. 4.9e-34; Indels 0; Gaps 0;
Matches 93; Conservative 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 21 EIVMQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 80
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWP 95
Db 81 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWP 115

RESULT 12
PL0106
IG kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VR>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <CRE>

Query Match 86.8%; Score 482; DB 2; Length 144;
Best Local Similarity 86.9%; Pred. No. 7.4e-34;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 21 EIVLTQSPATLSVSPGERATLSCRASQSVSYLAWYQQRPGQAPRLIIYDASNRATGIPA 80
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107
Db 81 RFGSGSGTEFTLTISLSLEPEDFAVYYCQQRNWLPTFGGTKVEIK 127

RESULT 13
JE0243
IG kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPIB, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243

A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 481; DB 2; Length 215;
Best Local Similarity 86.9%; Pred. No. 1.3e-33;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVATNVVMQKLGQAPRLIIYDASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYYCQHNWNPRTFGQTKVETK 107

RESULT 14
D30601
IG kappa chain V-III region (Cur) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: D30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: D30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 473.5; DB 2; Length 109;
Best Local Similarity 86.1%; Pred. No. 3e-33;
Matches 93; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYGASSRATGIP 60
QY 60 ARPSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107
Db 61 DRFGSGSGTDFTLTISLSEPEDFAVYYCQYGVSSPRTFGQTKVEIK 108

RESULT 15
PH0868
IG kappa chain V region (anti-DNA, II-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0868
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0868
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Note: the authors translated the codon CTC for residue 73 as Phe
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2

F;57-88/Region: framework 3

F:37-88/Region: Framework 3
F:89-95/Region: complementarity-determining 3

Query Match 85.2%; Score 473; DB 2; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.9e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	Db
1	1
EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA	EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPV
60	60

Qy 61 RPSGGSGTGTEFTLTISLSQSEDFAYVYCQQYNWP 95
| | | | | : | | | | |
Dd 61 RISGGSGTGTEFTLTISLSQSEDFAYVYCOEYNWP 95

Search completed: November 16, 2005, 22:04:06
Job time : 12.7849 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-6

Perfect score: 555

Sequence: 1 E1VMTQSPATLSVSPGERAT.....CQYNNWPRTFGGKTVEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	524.5	94.5	129	1 KV3H HUMAN	P04207 homo sapien
2	513	92.4	108	2 Q9UL83	Q9ul83 homo sapien
3	508.5	91.6	109	1 KV3F HUMAN	P01624 homo sapien
4	505.5	91.1	109	2 Q9UL85	Q9ul85 homo sapien
5	495.5	89.3	235	2 Q6GMW0	Q6gmw0 homo sapien
6	472.5	85.1	129	1 KV3L HUMAN	P18135 homo sapien
7	467.5	84.2	109	1 KV3B HUMAN	P01620 homo sapien
8	461.5	83.2	109	1 KV3D HUMAN	P01622 homo sapien
9	460.5	83.0	109	1 KV3E HUMAN	P01623 homo sapien
10	459.5	82.8	129	1 KV3M HUMAN	P18136 homo sapien
11	451.5	81.4	109	2 Q9UL78	Q9ul78 homo sapien
12	442.5	79.7	109	1 KV3C HUMAN	P04206 homo sapien
13	439.5	79.2	108	1 KV3A HUMAN	P01619 homo sapien
14	438	78.9	115	1 KV3I HUMAN	P04433 homo sapien
15	436.5	78.6	235	2 Q6GMV9	Q6gmv9 homo sapien
16	434.5	78.3	235	2 Q6RUF2	Q6rpf2 homo sapien
17	434	78.2	128	1 KV3K HUMAN	P06311 homo sapien
18	432	77.8	108	1 KV1M HUMAN	P01605 homo sapien
19	432	77.8	236	2 Q6PIL8	Q6pil8 homo sapien
20	431	77.7	236	2 Q6P5S8	Q6p5s8 homo sapien
21	428.5	77.2	109	2 Q9UL86	Q9ul86 homo sapien
22	422	76.0	108	2 Q9UL79	Q9ul79 homo sapien
23	418	75.3	134	1 KV4C HUMAN	P06314 homo sapien
24	415.5	74.9	116	1 KV3J HUMAN	P04434 homo sapien
25	408	73.5	114	1 KV4A HUMAN	P01625 homo sapien
26	407	73.3	108	2 Q9UL70	Q9ul70 homo sapien
27	407	73.3	236	2 Q6GMW1	Q6gmw1 homo sapien
28	405	73.0	108	1 KV1R HUMAN	P01610 homo sapien
29	405	73.0	236	2 Q6PIH7	Q6pih7 homo sapien
30	405	73.0	236	2 Q6PIT5	Q6pit5 homo sapien
31	404.5	72.9	100	1 KV3C_HUMAN	P01621 homo sapien

32	403	72.6	234	2	Q7Z473	Q7z473 homo sapien
33	402.5	72.5	133	1	KV4B_HUMAN	P06313 homo sapien
34	402	72.4	108	1	KV1G_HUMAN	P01599 homo sapien
35	400	72.1	108	1	KV1F_HUMAN	P01598 homo sapien
36	400	72.1	108	1	KV1V_HUMAN	P04430 homo sapien
37	400	72.1	236	2	Q7Z3Y4	Q7z3y4 homo sapien
38	400	72.1	244	2	Q6SZC8	Q6szc8 homo sapien
39	397	71.5	108	1	KV1L_HUMAN	P01604 homo sapien
40	396	71.4	236	2	Q6GMX8	Q6gmx8 homo sapien
41	395	71.2	240	2	Q6SZC9	Q6szc9 homo sapien
42	394	71.0	255	2	Q6KB05	Q6kb05 mus musculus
43	393	70.8	108	1	KV1K_HUMAN	P01603 homo sapien
44	393	70.8	108	1	KV1Q_HUMAN	P01609 homo sapien
45	393	70.8	236	2	Q6GMX9	Q6gmx9 homo sapien

ALIGNMENTS

RESULT 1

ID	KV3H HUMAN	STANDARD;	PRT;	129 AA.
AC	P04207;			
DT	20-MAR-1987 (Rel. 04, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-III region CLL precursor (Rheumatoid factor).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86177570; PubMed=3083417;			
RA	Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,			
RA	Goldfien R., Carson D.A.;			
RT	"Cloning and sequence determination of a human rheumatoid factor			
RT	light-chain gene."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).			
CC	-----			
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CC	-----			
DR	EMBL; M12740; AA58992.1; -.			
DR	HSSP; P01625; ILV6.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 129			
FT	DOMAIN 21 43			
FT	DOMAIN 44 54			
FT	Complementarity-determining-1.			
FT	Framework-2.			
FT	DOMAIN 55 69			
FT	DOMAIN 70 76			
FT	Complementarity-determining-2.			
FT	DOMAIN 77 108			
FT	DOMAIN 109 118			
FT	DOMAIN 119 129			
FT	Complementarity-determining-3.			
FT	JK1 segment.			
FT	DISULFID 43 108			
FT	By similarity.			
FT	NON_TER 129 129			
SQ	SEQUENCE 129 AA; 14275 MW; 5C13B411B560CC14 CRC64;			

Query Match

94.5%; Score 524.5; DB 1; Length 129;

```
Best Local Similarity 95.4%; Pred. No. 3.4e-47;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 80
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 81 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 128

RESULT 2
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P01625; 1LVE.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 92.4%; Score 513; DB 2; Length 108;
Best Local Similarity 93.5%; Pred. No. 4.5e-46;
Matches 100; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 107

RESULT 3
KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region P0M.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Best Local Similarity 95.4%; Pred. No. 3.4e-47;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

RN SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive Igm anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
globulin activity.
DR PIR; A01897; K3HUPM.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 91.6%; Score 508.5; DB 1; Length 109;
Best Local Similarity 91.7%; Pred. No. 1.3e-45;
Matches 99; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIP 59
DB 1 EIVMTQSPVTLSPGERATLSCRASQSVSNLAWYQKPGSGRLLIYGASTRATGIP 60
QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 61 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 108

RESULT 4
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSSP; P01625; 1LEK3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 91.1%; Score 505.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.8e-45;
Matches 99; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
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QY 1 EIVMTOSPATLSVSGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTOSPATLSVSGERATLSCWASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
Db 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 108

RESULT 5
Q6GMW0 PRELIMINARY; PRT; 235 AA.
AC O6GMW0;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

Query Match 89.3%; Score 495.5; DB 2; Length 235;
Best Local Similarity 88.9%; Pred. No. 7.6e-44;
Matches 96; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTOSPATLSVSGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 21 EIVMTOSPATLSVSGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPG 80

QY 1 EIVMTOSPATLSVSGERATLSCRASQSVSN- LAYYQKPGQAPRLIIYGASTRATGIP 59
Db 21 EIVLTQSPCTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGHSSRATGIP 80

QY 60 RFPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
Db 81 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPRTFGQGTKEIK 128

RESULT 7.
KV3B_HUMAN STANDARD; PRT; 109 AA.
ID KV3B_HUMAN
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 128

RESULT 6
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P10022; K3HUHA.
DR HSSP; P01625; 1BQO.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JKI segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5292772774D0 CRC64;

Query Match 85.1%; Score 472.5; DB 1; Length 129;
Best Local Similarity 86.1%; Pred. No. 9.9e-42;
Matches 93; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTOSPATLSVSGERATLSCRASQSVSN- LAYYQKPGQAPRLIIYGASTRATGIP 59
Db 21 EIVLTQSPCTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGHSSRATGIP 80

QY 60 RFPSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
Db 81 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPRTFGQGTKEIK 128

RESULT 7.
KV3B_HUMAN STANDARD; PRT; 109 AA.
ID KV3B_HUMAN
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 84.2%; Score 467.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 2.7e-41;
Matches 91; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTFGQGTKVELK 108

RESULT 8
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID KV3D_HUMAN
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region fi.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 83.2%; Score 461.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 1.2e-40;
Matches 91; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTFGQGTKVELK 108

RESULT 9
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01896; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 83.0%; Score 460.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 1.5e-40;
Matches 91; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCASQSVSN-N-LAWYQQKPGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSTFGQGTKVEIK 108

RESULT 10

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KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 187:840-852(1988).
CC -I- DISEASE: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.
DR PIR: P10021; K3HUHI.
DR HSSP: P01625; 1EEQ.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 21 44 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JKI segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 82.8%; Score 459.5; DB 1; Length 129;
Best Local Similarity 84.3%; Pred. No. 2.3e-40;
Matches 91; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN-N-LAWYQKPGQAPRLIYGASTRATGIP 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSV-LAWYQKPGQAPRLIYGASSRATGIP 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQYQYSSPWFEGGTKVEIK 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q9UL78 PRELIMINARY; PRT; 109 AA.
ID Q9UL78
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR PIR: A30601; A30601.
DR PIR: A30608; A30608.
DR PIR: B30601; B30601.
DR PIR: B30607; B30607.
DR PIR: C30601; C30601.
DR PIR: C30607; C30607.
DR PIR: C30608; C30608.
DR PIR: D30601; D30601.
DR PIR: D30607; D30607.
DR PIR: D30608; D30608.
DR PIR: F30607; F30607.
DR PIR: F30608; F30608.
DR PIR: G30601; G30601.
DR PIR: G30608; G30608.
DR PIR: H30607; H30607.
DR PIR: H44151; H44151.
DR PIR: I30601; I30601.
DR PIR: PH0963; PH0963.
DR PIR: PH0964; PH0964.
DR PIR: PH0965; PH0965.
DR PIR: S33988; S33988.
DR PIR: S34096; S34096.
DR HSSP: P01625; 1EK3.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 81.4%; Score 451.5; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.3e-39;
Matches 90; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN-N-LAWYQKPGQAPRLIYGASTRATGIP 59
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Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSV-LAWYQKPGQAPRLIYGASSRATGIP 60
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QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQYQYSSPWFEGGTKVEIK 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
KV3G_HUMAN STANDARD; PRT; 109 AA.
ID KV3G_HUMAN
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
rheumatoid factor of the wa idiotype group, in part predicted by its
reactivity with anti-peptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
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DR PIR; A01893; K3HUGO.
DR HSSP; P01625; 1EK3.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 79.7%; Score 442.5; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.2e-38;
Matches 87; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN--LAWYQOKPGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRAALLSRGVLAWYQOKPGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPRSFGGKVEIK 108

RESULT 13
KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA PubMed=11946339;
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6."
RL FEBS Lett. 2:301-304(1969).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSSP; P01625; 1EEQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 79.2%; Score 439.5; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 2.4e-38;
Matches 83; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

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Db 1 ZIVLTSPGTLSPGZRAALSCRAQLSGNYLAWYQOKPGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
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RESULT 14
KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Fecht M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within
the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01668; -; NOT ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P01625; 1EEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-III region VG.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 115 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 78.9%; Score 438; DB 1; Length 115;
Best Local Similarity 88.4%; Pred. No. 3.7e-38;
Matches 84; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Db 21 EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIIYDASNRATGIP 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWP 95
Db 81 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQRSNWP 115

RESULT 15
Q6GMV9 PRELIMINARY; PRT; 235 AA.
ID Q6GMV9
AC Q6GMV9;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073793; AAH73793.1; -
DR InterPro: IPR003599; Ig-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-set; 1.
DR Pfam: PF00047; ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 78.6%; Score 436.5; DB 2; Length 235;
Best Local Similarity 80.6%; Pred. No. 1.2e-37;
Matches 87; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

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DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
21 EIVLTQSPGTLISLSPGERAALSCRASQSVNSKYLAWYQKPGQAPRLMYAASIRATGIP 80
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPRFTGGTKVEIK 107
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 DRFSGSGSGTDFTLTISRLESEDFALYFCQYGTSTPLTFGGTKVEIK 128

Search completed: November 16, 2005, 22:01:50
Job time : 59.9908 secs

(028) 233 15 1700 0000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-6
Perfect score: 555
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNNWPRTFGQGTKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529.5	95.4	117	4	US-09-203-768A-4
2	498	89.7	224	4	US-09-456-090A-82
3	498	89.7	224	4	US-09-456-090A-88
4	498	89.7	224	4	US-09-456-090A-90
5	498	89.7	224	4	US-09-453-234-82
6	498	89.7	224	4	US-09-453-234-88
7	498	89.7	224	4	US-09-453-234-90
8	495	89.2	224	4	US-09-456-090A-36
9	495	89.2	224	4	US-09-453-234-36
10	485	87.4	224	4	US-09-456-090A-84
11	485	87.4	224	4	US-09-453-234-84
12	484	87.2	224	4	US-09-456-090A-46
13	484	87.2	224	4	US-09-453-234-46
14	475	85.6	106	4	US-08-535-109-8
15	475	85.6	106	4	US-08-844-215-11
16	471.5	85.0	109	3	US-09-025-769B-16
17	471.5	85.0	109	4	US-09-490-070A-16
18	471.5	85.0	109	4	US-09-490-153-16
19	471.5	85.0	109	4	US-09-490-324-16
20	470.5	84.8	110	3	US-09-025-769B-30
21	470.5	84.8	110	3	US-09-025-769B-47
22	470.5	84.8	110	4	US-09-490-070A-30
23	470.5	84.8	110	4	US-09-490-070A-47
24	470.5	84.8	110	4	US-09-490-153-30
25	470.5	84.8	110	4	US-09-490-153-47
26	470.5	84.8	110	4	US-09-490-324-30
27	470.5	84.8	110	4	US-09-490-324-47

28	467	84.1	234	3	US-09-049-672A-6	Sequence 6, Appli
29	463.5	83.5	108	2	US-08-232-081B-42	Sequence 42, Appl
30	463	83.4	107	4	US-09-438-954-40	Sequence 40, Appl
31	462	83.2	107	1	US-08-107-669D-14	Sequence 14, Appl
32	462	83.2	107	1	US-08-472-788A-14	Sequence 14, Appl
33	462	83.2	107	2	US-08-477-531B-14	Sequence 14, Appl
34	462	83.2	107	2	US-08-082-842A-14	Sequence 14, Appl
35	460.5	83.0	108	1	US-07-634-278-86	Sequence 86, Appl
36	460.5	83.0	108	1	US-08-477-728-86	Sequence 86, Appl
37	460.5	83.0	108	1	US-08-474-040-86	Sequence 86, Appl
38	460.5	83.0	108	1	US-08-487-200-86	Sequence 86, Appl
39	460.5	83.0	108	1	US-08-488-113B-150	Sequence 150, App
40	460.5	83.0	108	1	US-08-477-484B-150	Sequence 150, App
41	460.5	83.0	108	2	US-08-646-360-150	Sequence 150, App
42	460.5	83.0	108	3	US-08-839-765-150	Sequence 150, App
43	460.5	83.0	108	3	US-09-136-389-150	Sequence 150, App
44	460.5	83.0	108	3	US-08-484-537-86	Sequence 86, Appl
45	460.5	83.0	108	3	US-09-610-838-150	Sequence 150, App

ALIGNMENTS

RESULT 1
US-09-203-768A-4
; Sequence 4, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-4

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Best Local Similarity	96.3%	Pred. No. 3.8e-40;		
Matches 104;	Conservative 2;	Mismatches 1;	Indels 1;	Gaps 1;
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DB	9	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA	68	
QY	61	RFGSGSGTFTLTISLSQSEDFAVYCOQYNNW-PRTEGQGTKEIK	107	
DB	69	RFGSGSGTFTLTISLSQSEDFAVYCOQYNNWPPYTGQGTKEIK	116	
RESULT 2				
US-09-456-090A-82				
; Sequence 82, Application US/09456090A				
; Patent No. 6680209				
; GENERAL INFORMATION:				
; APPLICANT: Buechler, Joe				
; APPLICANT: Valkirs, Gunars				
; APPLICANT: Gray, Jeff				
; APPLICANT: Lonberg, Nils				
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS				
; FILE REFERENCE: 020015-000200US				
; CURRENT APPLICATION NUMBER: US/09/456,090A				
; CURRENT FILING DATE: 1999-12-06				
; NUMBER OF SEQ ID NOS: 110				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 82				
; LENGTH: 224				

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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQRTNWPRTFGGTKVEIK 107

RESULT 5
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTOSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLLIYGASTRATGIPA 60
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Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQRTNWPRTFGGTKVEIK 107

RESULT 6
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-88

; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
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Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQRTNWPRTFGGTKVEIK 107

RESULT 3
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTOSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLLIYGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTOSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQRTNWPRTFGGTKVEIK 107

RESULT 4
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
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; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-14L
US-09-453-234-88

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRNWPRTFGGTKVEIK 107

RESULT 7
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRNWPRTFGGTKVEIK 107

RESULT 8
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match      89.2%; Score 495; DB 4; Length 224;
Best Local Similarity 88.8%; Pred. No. 8.9e-37;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRNWPRTFGGTKVEIK 107

RESULT 9
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-36

Query Match      89.2%; Score 495; DB 4; Length 224;
Best Local Similarity 88.8%; Pred. No. 8.9e-37;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRNWPRTFGGTKVEIK 107

RESULT 10
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
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; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match 87.4%; Score 485; DB 4; Length 224;
Best Local Similarity 87.9%; Pred. No. 6.9e-36;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAAGIPA 60

QY 61 RFSGSGGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGGTFTLTISLSLEPEDFAVYCCQYNNWPLTFGGTKVEIK 107

RESULT 11

US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match 87.4%; Score 485; DB 4; Length 224;
Best Local Similarity 87.9%; Pred. No. 6.9e-36;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60
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QY 61 RFSGSGGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGGTFTLTISLSLEPEDFAVYCCQYNNWPLTFGGTKVEIK 107

RESULT 12

US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A

; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-456-090A-46

Query Match 87.2%; Score 484; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 8.5e-36;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAATGIPA 60

QY 61 RFSGSGGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGGTFTLTISLSLEPEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 13

US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match 87.2%; Score 484; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 8.5e-36;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60
Db 1 DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAATGIPA 60

QY 61 RFSGSGGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGGTFTLTISLSLEPEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 14

US-08-635-109-8
; Sequence 8, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
; APPLICANT: Persson, Mats A. A.
; APPLICANT: Allander, Tobias E.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:


```

; ADDRESSEE: REED & ROBINS
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,109
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCracken, Thomas P
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 2300-6146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-635-109-8

Query Match      85.6%; Score 475; DB 4; Length 106;
Best Local Similarity 86.5%; Pred. No. 2.4e-35;
Matches 90; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

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QY      64 GSGSGTEFTLTISLSQSEDFAVYYCQQYNWPRTEFGGQTKVEIK 107
Db      63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGQTKVEFK 106

Search completed: November 16, 2005, 22:07:18
Job time : 19.1939 secs

; ADDRESSEE: REED & ROBINS
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,109
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCracken, Thomas P
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 2300-6146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-635-109-8

Query Match      85.6%; Score 475; DB 4; Length 106;
Best Local Similarity 86.5%; Pred. No. 2.4e-35;
Matches 90; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      4 MTQSPATLSVSPGERATLSCRASQSVNNLAWYQQKPGQAPRLIYGASTRATGIPARFS 63
Db      3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLIYGGNTRATGTPDRFS 62

QY      64 GSGSGTEFTLTISLSQSEDFAVYYCQQYNWPRTEFGGQTKVEIK 107
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RESULT 15
US-08-844-215-11
; Sequence 11, Application US/08844215
; Patent No. 6747136
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 80146.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-844-215-11

Query Match      85.6%; Score 475; DB 4; Length 106;
Best Local Similarity 86.5%; Pred. No. 2.4e-35;
Matches 90; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      4 MTQSPATLSVSPGERATLSCRASQSVNNLAWYQQKPGQAPRLIYGASTRATGIPARFS 63
Db      3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLIYGGNTRATGTPDRFS 62

QY      64 GSGSGTEFTLTISLSQSEDFAVYYCQQYNWPRTEFGGQTKVEIK 107
Db      63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGQTKVEFK 106

Search completed: November 16, 2005, 22:07:18
Job time : 19.1939 secs
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(CNS) 2007-2008

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-6
Perfect score: 555
Sequence: 1 E1WMTQSPATLSVSPGERAT.....COQYNNWPRTFCQGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
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 - 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep.*
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 - 19: /cgn2_6/prodata/1/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
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 - 22: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	14	US-10-330-613-6
2	555	100.0	107	14	US-10-330-530-6
3	555	100.0	107	16	US-10-660-357-6
4	546	98.4	107	14	US-10-330-613-34
5	546	98.4	107	14	US-10-330-530-34
6	546	98.4	107	16	US-10-660-357-34
7	543	97.8	107	15	US-10-251-085B-122
8	543	97.8	107	16	US-10-737-252-122
9	539	97.1	107	15	US-10-251-085B-126
10	539	97.1	107	16	US-10-737-252-126
11	536	96.6	107	15	US-10-251-085B-109
Sequence 6, Appli					
Sequence 6, Appli					
Sequence 6, Appli					
Sequence 34, Appl					
Sequence 34, Appl					
Sequence 122, App					
Sequence 126, App					
Sequence 126, App					
Sequence 109, App					

12	536	96.6	107	15	US-10-251-085B-123	Sequence 123, App
13	536	96.6	107	16	US-10-737-252-109	Sequence 109, App
14	536	96.6	107	16	US-10-737-252-123	Sequence 123, App
15	536	96.6	107	17	US-10-727-155-310	Sequence 310, App
16	536	96.6	107	17	US-10-727-155-313	Sequence 313, App
17	536	96.6	107	18	US-10-901-736-2	Sequence 2, Appli
18	534	96.2	107	15	US-10-251-085B-117	Sequence 117, App
19	534	96.2	107	16	US-10-737-252-117	Sequence 117, App
20	533.5	96.1	108	15	US-10-251-085B-132	Sequence 132, App
21	533.5	96.1	108	16	US-10-737-252-132	Sequence 132, App
22	533	96.0	107	15	US-10-251-085B-119	Sequence 119, App
23	533	96.0	107	16	US-10-737-252-119	Sequence 119, App
24	533	96.0	107	17	US-10-727-155-314	Sequence 314, App
25	533	96.0	107	17	US-10-938-353-107	Sequence 107, App
26	532.5	95.9	108	18	US-10-984-960A-29	Sequence 29, Appl
27	532	95.9	250	10	US-09-880-748-1952	Sequence 1952, Ap
28	532	95.9	250	15	US-10-293-418-1952	Sequence 1952, Ap
29	529.5	95.4	117	14	US-10-300-675-4	Sequence 4, Appli
30	529.5	95.4	117	14	US-10-300-675-42	Sequence 42, Appl
31	529.5	95.4	117	14	US-10-300-675-44	Sequence 44, Appl
32	529.5	95.4	117	14	US-10-300-675-46	Sequence 46, Appl
33	529.5	95.4	117	17	US-10-910-124-4	Sequence 4, Appli
34	529	95.3	246	10	US-09-880-748-1268	Sequence 1268, Ap
35	529	95.3	246	15	US-10-293-418-1268	Sequence 1268, Ap
36	528	95.1	107	15	US-10-251-085B-115	Sequence 115, App
37	528	95.1	107	16	US-10-737-252-115	Sequence 115, App
38	526	94.8	107	15	US-10-308-817-124	Sequence 124, App
39	526	94.8	107	15	US-10-453-698-124	Sequence 124, App
40	525	94.6	107	17	US-10-727-155-146	Sequence 146, App
41	525	94.6	107	17	US-10-727-155-184	Sequence 184, App
42	525	94.6	127	15	US-10-309-764-137	Sequence 137, App
43	524.5	94.5	106	17	US-10-727-155-277	Sequence 277, App
44	524	94.4	154	16	US-10-665-383-82	Sequence 82, Appl
45	523.5	94.3	108	17	US-10-893-576-182	Sequence 182, App

ALIGNMENTS

RESULT 1
US-10-330-613-6
; Sequence 6, Application US/10330613
; Publication NO. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-6

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	E1WMTQSPATLSVSPGERATLSCRASQSVNNLAWYQOKPGQAPRLLIYGASTRATGIPA	60
Db	1	E1WMTQSPATLSVSPGERATLSCRASQSVNNLAWYQOKPGQAPRLLIYGASTRATGIPA	60
Qy	61	RFSGSGSGTEFTLTISSLQSEDPFVYCCQYNNWPRTFCQGTKVEIK	107
Db	61	RFSGSGSGTEFTLTISSLQSEDPFVYCCQYNNWPRTFCQGTKVEIK	107

RESULT 2

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US-10-330-530-6
; Sequence 6, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-6

Query Match      100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 3
US-10-660-357-6
; Sequence 6, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX 030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-6

Query Match      100.0%; Score 555; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 4
US-10-330-613-34
; Sequence 34, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
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; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-34

Query Match      98.4%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 5
US-10-330-530-34
; Sequence 34, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-34

Query Match      98.4%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 6
US-10-660-357-34
; Sequence 34, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX 030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
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; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-126

Query Match          97.1%; Score 539; DB 16; Length 107;
Best Local Similarity 97.2%; Pred. No. 6.8e-39;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 11
US-10-251-085B-109
; Sequence 109, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-109

Query Match          96.6%; Score 536; DB 15; Length 107;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 12
US-10-251-085B-123
; Sequence 123, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
```

```
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-123

Query Match          96.6%; Score 536; DB 15; Length 107;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 13
US-10-737-252-109
; Sequence 109, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-109

Query Match          96.6%; Score 536; DB 16; Length 107;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 14
US-10-737-252-123
; Sequence 123, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
```

APPLICANT: Bowdish, Katherine S.
APPLICANT: Fredrickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21 CIP
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 10/251,085
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.2
SEQ ID NO 123
LENGTH: 107
TYPE: PRT
ORGANISM: human
US-10-737-252-123

Query Match 96.6%; Score 536; DB 16; Length 107;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNWYQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSLOSEDFAVYVCOQYNNWPRTFGQGTKEIK 107
DB 61 RFGSGSGTFTLTITSSLOSEDFAVYVCOQYNNWPRTFGQGTKEIK 107

RESULT 15
US-10-727-155-310
Sequence 310, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniwami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchao
APPLICANT: Raffaela Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 310
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-310

Query Match 96.6%; Score 536; DB 17; Length 107;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNWYQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSLOSEDFAVYVCOQYNNWPRTFGQGTKEIK 107
DB 61 RFGSGSGTFTLTITSSLOSEDFAVYVCOQYNNWPRTFGQGTKEIK 107

Search completed: November 16, 2005, 23:05:40
Job time : 66.6949 secs

(CNC) 2000-0000-0000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 62.5147 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-10
Perfect score: 566
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPESFGQGTKLEIK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	100.0	109	7 ADC99781	Adc99781 Anti-huma
2	566	100.0	109	7 ADD05385	Add05385 Anti-MUC1
3	566	100.0	109	7 ADF09823	Adf09823 Human ant
4	520	91.9	108	8 ADP47299	Adp47299 Human pho
5	520	91.9	214	8 ADR23360	Adr23360 Human CD7
6	520	91.9	214	8 ADR23358	Adr23358 Human CD7
7	520	91.9	214	8 ADR23366	Adr23366 Human CD7
8	520	91.9	214	8 ADR23364	Adr23364 Human CD7
9	519.5	91.8	237	3 AAY96298	Aay96298 Human IGF
10	519	91.7	108	8 ADP47103	Adp47103 Human pho
11	517	91.3	108	8 ADP47113	Adp47113 Human pho
12	515.5	91.1	237	3 AAY96289	Aay96289 Human IGF
13	512	90.5	107	8 ADP22402	Adp22402 Human ant
14	512	90.5	108	8 ADP47294	Adp47294 Human pho
15	512	90.5	132	2 AAW22842	Aaw22842 Human ant
16	511	90.3	105	8 ADR47411	Adr47411 Human ger
17	511	90.3	108	6 ABP96009	Abp96009 HSA antib
18	511	90.3	108	6 ADL92386	Adl92386 Anti-HSA
19	511	90.3	108	8 ADQ14601	Adq14601 Single-d
20	511	90.3	108	8 ADQ77191	Adq77191 Dummy VK
21	511	90.3	108	8 ADQ77181	Adq77181 VK dummy
22	511	90.3	108	8 ADQ90912	Adq90912 Vb/Ck pro
23	511	90.3	108	8 ADS78333	Ads78333 vkappa du
24	511	90.3	108	8 ADS78331	Ads78331 Dkappa9-
25	511	90.3	240	2 AAY02472	Aay02472 A single

26	511	90.3	240	4 AAB46007	Aab46007 Human MUC
27	511	90.3	240	4 AAB46038	Aab46038 Human TF
28	511	90.3	240	4 AAB46008	Aab46008 Human MUC
29	511	90.3	240	4 AAB46006	Aab46006 Human MUC
30	511	90.3	240	4 AAB46005	Aab46005 Human MUC
31	511	90.3	240	6 ABP95997	Abp95997 Human eer
32	511	90.3	240	8 ADL92369	Adl92369 Human pha
33	510	90.3	249	8 ADQ77185	Adq77185 HSA Heavy
34	510	90.1	249	8 ADR23322	Adr23322 Human CD7
35	510	90.1	249	8 ADR23326	Adr23326 Human CD7
36	509	89.9	108	6 AAO16706	Aao16706 Human ant
37	509	89.9	108	8 ADP47107	Adp47107 Human pho
38	508.5	89.8	111	8 ADP47305	Adp47305 Human pho
39	506	89.4	107	2 AAW16649	Aaw16649 Anti-canc
40	505.5	89.3	108	4 AAG93589	Aag93589 Human ant
41	505.5	89.3	108	4 AAG93600	Aag93600 Human ant
42	505.5	89.3	108	6 ABO27407	Abo27407 Anti-Rh(D
43	505.5	89.3	108	6 ABO27396	Abo27396 Anti-Rh(D
44	505.5	89.3	111	8 ADP47306	Adp47306 Human pho
45	505	89.2	107	4 AAG65567	Aag65567 Amino aci

ALIGNMENTS

RESULT 1
ADC99781
ID ADC99781 standard; protein; 109 AA.
XX
AC ADC99781;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 10.
XX

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
cytotoxic; melanoma; oesophageal; pancreatic; colorectal tumour;
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
lung cancer; human.
XX

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55.

N-PSDB; ADC99783.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 10; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising
a heavy or light chain amino acid or a heavy or light chain variable
domain where the antibody binds to MUC18. The monoclonal antibody of the
invention demonstrates cytostatic activity and may be useful for treating
a disease or condition associated with the expression of MUC18 on the
cell surface such as tumours, specifically melanoma, oesophageal,
pancreatic or colorectal tumours, carcinomas, particularly cervical
carcinomas and cervical intraepithelial neoplasia and cancers including
colorectal, breast or lung cancer, as well as other malignancies. The
current sequence is that of the anti-human MUC18 monoclonal antibody

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CC light chain protein of the invention.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

RESULT 2
ADD05385
ID ADD05385 standard; protein; 109 AA.
XX
AC ADD05385;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 10.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
DR N-PSDB; ADD05387.
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 10; 87pp; English.
XX
PS The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

RESULT 3
ADF09823
ID ADF09823 standard; protein; 109 AA.
XX
AC ADF09823;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #3.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
DR N-PSDB; ADF09825.
XX

Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 10; 83pp; English.
XX
PS The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
```

RESULT 4

ADP47299
 ID ADP47299 standard; protein; 108 AA.
 XX AC ADP47299;
 XX AC ADP47299;
 XX DT 09-SEP-2004 (first entry)
 XX DE Human phospholipase A2-specific monoclonal antibody light chain #19.
 XX DE human; monoclonal antibody; phospholipase A2; PLA2;
 XX DE inflammatory disorder; degenerative disorder;
 XX DE joint inflammatory reaction; skin inflammatory reaction;
 XX DE blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 XX DE Alzheimer's disease; atherosclerosis; restenosis; light chain.
 XX OS Homo sapiens.
 XX PN WO2004050850-A2.
 XX PD 17-JUN-2004.
 XX PF 02-DEC-2003; 2003WO-US038234.
 XX PR 02-DEC-2002; 2002US-0430724P.
 XX PA (ABGE-) ABGENIX INC.
 XX PA (LEXI-) LEXICON GENETICS, INC.
 XX PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 XX PI Jia X, Nocerini MR;
 XX DR WPI; 2004-461119/43.
 XX PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 XX PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 XX PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX PS Example 5; SEQ ID NO 214; 128pp; English.
 XX CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the light chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.
 XX SQ Sequence 108 AA;
 Query Match 91.9%; Score 520; DB 8; Length 108;
 Best Local Similarity 93.6%; Pred. No. 1.6e-29;
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWNWYQKPKAPKLLIYCASSLSQGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWNWYQKPKAPKLLIYCASSLSQGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCROSYSTPPCECSFGQGTKEIK 109
 DB 61 RFGSGSGTDFTLTISLQPEDFATYYCQOSYSTPP--TFGQGTKEIK 107
 RESULT 5
 ADR23360
 ID ADR23360 standard; protein; 214 AA.
 XX AC ADR23360;
 XX DT 04-NOV-2004 (first entry)

XX DE Human CD72-targeted IgG1 light chain.
 XX DE Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 XX KW immunosuppressive; cancer; autoimmune disease; gene therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 1..108
 FT /label= V_region
 FT Region 109..214
 FT /label= C_region
 XX PN WO2004067569-A1.
 XX PD 12-AUG-2004.
 XX PF 27-JAN-2003; 2003WO-EP050004.
 XX PR 27-JAN-2003; 2003WO-EP050004.
 XX PA (CRUC-) CRUCCELL HOLLAND BV.
 XX PI Bakker ABH, Marissen WE;
 XX DR WPI; 2004-580978/56.
 XX DR N-PSDB; ADR23359.
 XX PT New internalizing human binding molecules capable of specifically binding
 PT to CD72, useful for diagnosing and/or treating B-cell associated
 PT diseases, such as cancer or autoimmune disorders.
 XX PS Example 5; SEQ ID NO 52; 174pp; English.
 XX CC The present sequence is the protein sequence of the light chain of human
 CC IgG1 antibody 024, which specifically recognises human B cell associated
 CC antigen CD72. An scFv ADR23322 selected from an antibody phage display
 CC library was shown to specifically recognise the human CD72 receptor. The
 CC scFv was recloned in IGG expression vector C01 using primers designed to
 CC restore complete human frameworks, thereby generating antibody 024. Such
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
 CC as internalising human binding molecules of the invention. These
 CC internalising human binding molecules are capable of (specifically)
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
 CC associated with cells. Upon binding to CD72 present on the surface of
 CC target cells, the binding molecules internalise. In addition to the
 CC internalising human binding molecules, the invention provides
 CC immunconjugates comprising an internalising human binding molecule and a
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
 CC nucleic acids encoding these, and compositions comprising them. The
 CC internalising human binding molecule, immunconjugate, nucleic acid
 CC molecule or composition can be used in the diagnosis and/or treatment of
 CC a B cell associated disorder or disease, especially a B cell associated
 CC cancer and B cell associated autoimmune disorder (claimed).
 XX SQ Sequence 214 AA;
 Query Match 91.9%; Score 520; DB 8; Length 214;
 Best Local Similarity 93.6%; Pred. No. 2.9e-29;
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWNWYQKPKAPKLLIYCASSLSQGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWNWYQKPKAPKLLIYCASSLSQGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCROSYSTPPCECSFGQGTKEIK 109
 DB 61 RFGSGSGTDFTLTISLQPEDFATYYCQOSYSTPP--TFGQGTKEIK 107
 RESULT 6
 ADR23358

ID ADR23358 standard; protein; 214 AA.
 XX ADR23358;
 AC
 XX 04-NOV-2004 (first entry)
 DT Human CD72-targeted IgG1 light chain.
 XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Region 1..108
 FT /label= V_region
 FT Region 109..214
 FT /label= C_region
 XX WO2004067569-A1.
 PN
 XX 12-AUG-2004.
 PD
 XX 27-JAN-2003; 2003WO-EP050004.
 PF
 XX 27-JAN-2003; 2003WO-EP050004.
 PR
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Bakker ABH, Marissen WE;
 PI
 XX WPI; 2004-580978/56.
 DR N-PSDB; ADR23357.
 DR
 XX New internalizing human binding molecules capable of specifically binding
 PT to CD72, useful for diagnosing and/or treating B-cell associated
 PT diseases, such as cancer or autoimmune disorders.
 XX
 PS Example 5; SEQ ID NO 50; 174pp; English.
 XX
 CC The present sequence is the protein sequence of the light chain of human
 CC IgG1 antibody 004, which specifically recognises human B cell associated
 CC antigen CD72. An scFv ADR23320 selected from an antibody phage display
 CC library was shown to specifically recognise the human CD72 receptor. The
 CC scFv was recombined in IGG expression vector C01 using primers designed to
 CC restore complete human frameworks, thereby generating antibody 004. Such
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
 CC as internalising human binding molecules of the invention. These
 CC internalising human binding molecules are capable of (specifically)
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
 CC associated with cells. Upon binding to CD72 present on the surface of
 CC target cells, the binding molecules internalise. In addition to the
 CC internalising human binding molecules, the invention provides
 CC immunocombinates comprising an internalising human binding molecule and a
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
 CC nucleic acids encoding these, and compositions comprising them. The
 CC internalising human binding molecule, immunoconjugate, nucleic acid
 CC molecule or composition can be used in the diagnosis and/or treatment of
 CC a B cell associated disorder or disease, especially a B cell associated
 CC cancer and B cell associated autoimmune disorder (claimed).
 XX
 SQ Sequence 214 AA;
 Query Match 91.9%; Score 520; DB 8; Length 214;
 Best Local Similarity 93.6%; Pred. No. 2.9e-29;
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPGKAPKLLIYGASSLSQSGVPS 60
 QY 61 RFGSGSGTDFLTITSLQPEDFATYYCQOSYSTPP--TFQGQTKVEIK 109
 1
 Db 61 RFGSGSGTDFLTITSLQPEDFATYYCQOSYSTPP--TFQGQTKVEIK 107
 RESULT 7
 ADR23366
 ID ADR23366 standard; protein; 214 AA.
 XX ADR23366;
 AC
 XX 04-NOV-2004 (first entry)
 DT Human CD72-targeted IgG1 light chain.
 XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Region 1..108
 FT /label= V_region
 FT Region 109..214
 FT /label= C_region
 XX WO2004067569-A1.
 PN
 XX 12-AUG-2004.
 PD
 XX 27-JAN-2003; 2003WO-EP050004.
 PF
 XX 27-JAN-2003; 2003WO-EP050004.
 PR
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Bakker ABH, Marissen WE;
 PI
 XX WPI; 2004-580978/56.
 DR N-PSDB; ADR23365.
 DR
 XX New internalizing human binding molecules capable of specifically binding
 PT to CD72, useful for diagnosing and/or treating B-cell associated
 PT diseases, such as cancer or autoimmune disorders.
 XX
 PS Example 5; SEQ ID NO 58; 174pp; English.
 XX
 CC The present sequence is the protein sequence of the light chain of human
 CC IgG1 antibody 132, which specifically recognises human B cell associated
 CC antigen CD72. An scFv ADR23332 selected from an antibody phage display
 CC library was shown to specifically recognise the human CD72 receptor. The
 CC scFv was recombined in IGG expression vector C01 using primers designed to
 CC restore complete human frameworks, thereby generating antibody 132. Such
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
 CC as internalising human binding molecules of the invention. These
 CC internalising human binding molecules are capable of (specifically)
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
 CC associated with cells. Upon binding to CD72 present on the surface of
 CC target cells, the binding molecules internalise. In addition to the
 CC internalising human binding molecules, the invention provides
 CC immunocombinates comprising an internalising human binding molecule and a
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
 CC nucleic acids encoding these, and compositions comprising them. The
 CC internalising human binding molecule, immunoconjugate, nucleic acid
 CC molecule or composition can be used in the diagnosis and/or treatment of
 CC a B cell associated disorder or disease, especially a B cell associated
 CC cancer and B cell associated autoimmune disorder (claimed).
 XX
 SQ Sequence 214 AA;
 Query Match 91.9%; Score 520; DB 8; Length 214;
 Best Local Similarity 93.6%; Pred. No. 2.9e-29;
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPGKAPKLLIYGASSLSQSGVPS 60
 QY 61 RFGSGSGTDFLTITSLQPEDFATYYCQOSYSTPP--TFQGQTKVEIK 109
 1
 Db 61 RFGSGSGTDFLTITSLQPEDFATYYCQOSYSTPP--TFQGQTKVEIK 107

Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASLSQSGVPS 60
QY 61 RFGSGSGTFTLTISLSQPEDPATYVCROSYSYTPPSCSFQGTKEIK 109
Db 61 RFGSGSGTFTLTISLSQPEDPATYVCQSYSTPP--TFGQGTKEIK 107

RESULT 8
ADR23364
ID ADR23364 standard; protein; 214 AA.

XX ADR23364;

XX 04-NOV-2004 (first entry)

XX Human CD72-targeted IgG1 light chain.

XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
XX immunosuppressive; cancer; autoimmune disease; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Region I..108
XX FT /label= V_region
XX FT 109..214
XX FT /label= C_region

XX WO2004067569-A1.

XX 12-AUG-2004.

XX 27-JAN-2003; 2003WO-EP050004.

XX 27-JAN-2003; 2003WO-EP050004.

XX (CRUC-) CRUCCELL HOLLAND BV.

XX Bakker ABH, Marissen WE;

XX WPI; 2004-580978/56.

XX N-PSDB; ADR23363.

XX New internalizing human binding molecules capable of specifically binding
XX to CD72, useful for diagnosing and/or treating B-cell associated
XX diseases, such as cancer or autoimmune disorders.

XX Example 5; SEQ ID NO 56; 174pp; English.

XX The present sequence is the protein sequence of the light chain of human
XX IgG1 antibody 041, which specifically recognises human B cell associated
XX antigen CD72. An scFv ADR23330 selected from an antibody phage display
XX library was shown to specifically recognise the human CD72 receptor. The
XX scFv was recloned in IgG expression vector C01 using primers designed to
XX restore complete human frameworks, thereby generating antibody 041. Such
XX anti-CD72 immunoglobulins or their antigen-binding fragments can be used
XX as internalising human binding molecules of the invention. These
XX internalising human binding molecules are capable of (specifically)
XX binding to CD72 or its antigenic determinant, and preferably bind to CD72
XX associated with cells. Upon binding to CD72 present on the surface of
XX target cells, the binding molecules internalise. In addition to the
XX internalising human binding molecules, the invention provides
XX immunocjugates comprising an internalising human binding molecule and a
XX tag (toxic substance, radioactive substance, liposome and/or enzyme),
XX nucleic acids encoding these, and compositions comprising them. The
XX internalising human binding molecule, immunocjugate, nucleic acid
XX molecule or composition can be used in the diagnosis and/or treatment of
XX a B cell associated disorder or disease, especially a B cell associated
XX cancer and B cell associated autoimmune disorder (claimed).

XX Sequence 214 AA;

Query Match 91.9%; Score 520; DB 8; Length 214;
Best Local Similarity 93.6%; Pred. No. 2.9e-29;
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYGASLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASLSQSGVPS 60

QY 61 RFGSGSGTFTLTISLSQPEDPATYVCROSYSYTPPSCSFQGTKEIK 109
Db 61 RFGSGSGTFTLTISLSQPEDPATYVCQSYSTPP--TFGQGTKEIK 107

RESULT 9
AA96298

ID AA96298 standard; protein; 237 AA.

XX AA96298;

XX 16-AUG-2000 (first entry)

XX Human IGFAM-10 immunoglobulin.

XX Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
XX infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Peptide 1..22
XX FT /label= signal_peptide
XX FT 23..237
XX FT /label= IGFAM-10
XX FT 38..112
XX FT /label= Ig_domain
XX FT 150..219
XX FT /label= Ig_domain
XX FT 193..236
XX FT /label= Ig_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX Lu DM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27390.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX protein is useful for preventing and treating disorders associated with
XX altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 85-86; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein
XX IGFAM-10. Its gene was isolated from a cDNA library of colon tissue. It
XX is expressed in reproductive, gastrointestinal and cardiovascular tissue,
XX where cancer and inflammation are common. The gene, protein, its
XX antibodies, agonists and antagonists are suitable for diagnosing and
XX treating many diseases, including cancer, immune system disorders (such
XX as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,
XX atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,
XX emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,

CC rheumatoid arthritis, scleroderma, systemic lupus erythematosus and
 CC ulcerative colitis), complications of cancer, haemodialysis and
 CC extracorporeal circulation, trauma and haematopoietic cancer (such as
 CC leukaemia) and infections caused by bacteria, viruses, fungi or parasites
 XX
 SQ Sequence 237 AA;

Query Match 91.8%; Score 519.5; DB 3; Length 237;
 Best Local Similarity 93.6%; Pred. No. 3.4e-29;
 Matches 102; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
 Db 23 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 82
 Qy 61 RFSGSGSGTDFTLTIISSLOPEDFATYYCROSYSTPPESFGQGTKEIK 109
 Db 83 RFSGSGSGTDFTLTIISSLOPEDFATYYCQOSYSTPP--ITFGQGTKEIK 130

RESULT 10
 ADP47103
 ID ADP47103 standard; protein; 108 AA.
 AC ADP47103;
 XX 09-SEP-2004 (first entry)
 DT
 DE Human phospholipase A2-specific monoclonal antibody light chain #8.
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050850-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis.
 XX
 PS Claim 2; SEQ ID NO 18; 128pp; English.
 XX

The invention comprises a human monoclonal antibody that binds to
 phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 useful in the preparation of a medicament for the treatment of
 inflammatory and degenerative disorders stemming from inflammatory
 reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 amino acid sequence represents the light chain from a monoclonal antibody
 that is specific for the human phospholipase A2 (PLA2) enzyme.

Query Match 91.7%; Score 519; DB 8; Length 108;
 Best Local Similarity 93.6%; Pred. No. 1.8e-29;

Matches 102; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
 Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60
 Qy 61 RFSGSGSGTDFTLTIISSLOPEDFATYYCROSYSTPPESFGQGTKEIK 109
 Db 61 RFSGSGSGTDFTLTIISSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 11
 ADP47113
 ID ADP47113 standard; protein; 108 AA.
 AC ADP47113;
 XX 09-SEP-2004 (first entry)
 DT
 DE Human phospholipase A2-specific monoclonal antibody light chain #13.
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050850-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 amino acid sequence represents the light chain from a monoclonal antibody
 that is specific for the human phospholipase A2 (PLA2) enzyme.

Query Match 91.3%; Score 517; DB 8; Length 108;
 Best Local Similarity 92.7%; Pred. No. 2.6e-29;
 Matches 101; Conservative 5; Mismatches 1; Indels 2; Gaps 1;
 Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60
 Qy 61 RFSGSGSGTDFTLTIISSLOPEDFATYYCROSYSTPPESFGQGTKEIK 109
 Db 61 RFSGSGSGTDFTLTIISSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

Sequence 108 AA;

RESULT 12
ID AAY96289 standard; protein; 237 AA.
XX
AC AAY96289;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-1 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= signal_peptide
FT /label= IGFAM-1
FT Domain 38..112
FT /label= Ig_domain
FT Domain 150..219
FT /label= Ig_domain
FT Region 154..176
FT /label= Ig_signature
FT Domain 193..236
FT /label= Ig_domain
FT Region 215..232
FT /label= Ig_signature
XX
XX WO200029583-A2.
XX
XX 25-MAY-2000.
XX
XX 19-NOV-1999; 99WO-US027566.
XX
XX 19-NOV-1998; 98US-00195853.
XX
XX 22-DEC-1998; 98US-0113635P.
XX
XX 07-APR-1999; 99US-0128194P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX Lu DAM, Lal P, Hillman JL, Yang J;
XX
XX WPI; 2000-387796/33.
XX
XX N-PSDB; AAA27381.
XX
XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX protein is useful for preventing and treating disorders associated with
XX altered levels of the protein such as cancer, immune system disorders.
XX
XX Claim 1; Page 77-78; 105pp; English.
XX
XX The present sequence is the human immunoglobulin superfamily protein
XX IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane
XX tissue. It is expressed in reproductive, gastrointestinal and
XX cardiovascular tissue, where cancer and inflammation are common. The
XX gene, protein, its antibodies, agonists and antagonists are suitable for
XX diagnosing and treating many diseases, including cancer, immune system
XX disorders (such as inflammation, AIDS, allergies, anaemia,
XX arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX systemic lupus erythematosus and ulcerative colitis), complications of
XX cancer, haemodialysis and extracorporeal circulation, trauma and
XX haematopoietic cancer (such as leukaemia) and infections caused by
XX bacteria, viruses, fungi or parasites
XX
XX Sequence 237 AA;

Query Match 91.1%; Score 515.5; DB 3; Length 237;
Best Local Similarity 92.7%; Pred. No. 6.6e-29;
Matches 101; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY 1 DIQMTSPSSLSASVGDRTTITCRASQSI SNLYNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
DB 23 DIQMTSPSSLSASVGDRTTITCRAGQSI SNLYNWYQOKPGKAPKLLIYAASSLSQSGVPS 82
QY 61 RFSGSGSGTDTLTITSSLPQDPATYYCRQSYSTPPECSPFGQGTKEIK 109
DB 83 RFSGSGSGTDTLTITSSLPQDPATYYCQSYSTPP-ITFGQGTREIK 130
RESULT 13
ADP22402
ID ADP22402 standard; protein; 107 AA.
XX
AC ADP22402;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human anti-TNFA antibody light chain variable region SEQ ID NO:308.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX Homo sapiens.
XX
XX WO2004050683-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038281.
XX
XX 02-DEC-2002; 2002US-0430729P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
XX Manchulench K, Faggioni R, Senaldi G, Qiaojuan JS;
XX WPI; 2004-480601/45.
XX
XX New recombinant human monoclonal antibody that specifically binds to
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX arthritis.
XX
XX Example 10; SEQ ID NO 308; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (1) that
XX specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFA in a patient sample, comprising contacting with
XX (1), and detecting the level of binding between the antibody and TNFA in
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an

CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (1) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 90.5%; Score 512; DB 8; Length 107;
 Best Local Similarity 92.7%; Pred. No. 5.7e-29;
 Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60
 Qy 61 RFSGSGSGTDTLTITSSLPQDFATYYCROSYSSTPPECSCFOGKLEIK 109
 Db 61 RFSGSGSGTDTLTITSSLPQDFATYYCQOSYSTP--ITFGQGRLEIK 107

RESULT 14

ADP47294
 ID ADP47294 standard; protein; 108 AA.
 XX
 AC ADP47294;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human phospholipase A2-specific monoclonal antibody light chain #14.
 XX
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
 XX
 OS Homo sapiens.
 XX
 WO2004050850-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.

PS Example 5; SEQ ID NO 209; 128pp; English.
 XX The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the light chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 108 AA;

Query Match 90.5%; Score 512; DB 8; Length 108;
 Best Local Similarity 92.7%; Pred. No. 5.8e-29;
 Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60
 Qy 61 RFSGSGSGTDTLTITSSLPQDFATYYCROSYSSTPPECSCFOGKLEIK 109
 Db 61 RFSGSGSGTDTLTITSSLPQDFATYYCQOSYSTP--ITFGQGRLEIK 107

RESULT 15

AAW22842
 ID AAW22842 standard; protein; 132 AA.
 XX
 AC AAW22842;
 XX
 DT 12-SEP-1997 (first entry)
 XX
 DE Human anti-tumour antigen antibody light chain variable region.
 XX
 KW Human; tumour antigen; cancer; monoclonal; antibody; light chain;
 KW variable region; medicine; pharmacology; biochemistry; CDR;
 KW complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= sig_peptide
 FT Peptide 23..132
 FT /label= mat_peptide
 FT Region 46..56
 FT /label= CDR_1
 FT Region 72..78
 FT /label= CDR_2
 FT Region 111..119
 FT /label= CDR_3

JP09100300-A.

15-APR-1997.
 XX
 PF 03-OCT-1995; 95JP-00278266.
 XX
 PR 03-OCT-1995; 95JP-00278266.
 XX
 PA (HAGI/) HAGIWARA Y.
 XX
 DR WPI; 1997-276726/25.
 DR N-PSDB; AAT75423.
 XX
 PT Anticancer human monoclonal antibody variable region sequences - and
 PT related DNA and RNA.
 XX
 PS Claim 9; Page 11; 14pp; Japanese.
 XX

The present sequence is a human anti-tumour antigen monoclonal antibody

CC (Mab) light chain variable region, useful in medicine, pharmacology and
CC biochemistry. The isotype of a Mab secreted by the human/human hybridoma
CC Ht was determined to be mu and kappa. Human Mab was purified, and the
CC antigen recognised by human Mab CLN"-IgM identified by western blotting
XX
SQ Sequence 132 AA;

Query Match 90.5%; Score 512; DB 2; Length 132;
Best Local Similarity 92.7%; Pred. No. 6.9e-29;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQISNLYLNWYQOKPGKAPKLLIYGASSLQSGVPS 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
23 DIQMTQSPSSLSASVGRVTITCRASQISNLYLNWYQOKPGKAPKLLIYAASLQSGVPS 82
QY 61 RFSGSGSGTDFTLTISSLQPEDPATYCYCQSYSTPPECSPFGQGTKEIK 109
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
83 RFSGSGSGTDFTLTISSLQPEDPATYCYCQSYSTPQ--TFGQGTKEIK 129

Search completed: November 16, 2005, 21:51:37
Job time : 63.5147 secs

(CLASS) 2000 K. F. M. 1011

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.0239 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-10
Perfect score: 566
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPECSTFGQGTKLEIK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	90.3	123	2 S40331	Ig kappa chain - h
2	509	89.9	127	2 S40367	Ig kappa chain V-J
3	505	89.2	108	2 B49047	Ig kappa chain V r
4	502	88.7	120	2 S46370	Ig kappa chain V-J
5	500	88.3	129	2 S40317	Ig kappa chain - h
6	491	86.7	129	1 K1HUWK	Ig kappa chain pre
7	489	86.4	108	2 S44122	Ig kappa chain V r
8	489	86.4	108	2 S47182	Ig kappa chain - h
9	485	85.7	108	1 K1HUHU	Ig kappa chain V-I
10	484	85.5	109	2 S31981	Ig kappa chain - h
11	482	85.2	109	2 S31998	Ig kappa chain - h
12	482	85.2	122	2 S40314	Ig kappa chain - h
13	480.5	84.9	107	2 S36275	Ig kappa chain V r
14	476	84.1	129	2 S52793	Ig kappa chain V r
15	475	83.9	117	2 S24206	Ig kappa chain V r
16	474	83.7	108	2 S19674	Ig kappa chain V r
17	473	83.6	122	2 S40370	Ig kappa chain - h
18	472.5	83.5	125	2 S40315	Ig kappa chain - h
19	468	82.7	116	2 A27594	Ig kappa chain pre
20	467	82.5	129	2 S52792	Ig kappa chain V r
21	466	82.3	107	2 S36264	Ig kappa chain V r
22	466	82.3	107	2 S36269	Ig kappa chain V
23	466	82.3	109	2 S31979	Ig kappa chain - h
24	465	82.2	108	2 S31977	Ig kappa chain - h
25	465	82.2	110	2 S44118	Ig kappa chain V-J
26	464.5	82.1	106	2 PC2397	anti-tetanus toxin
27	462	81.6	109	2 S31980	Ig kappa chain - h
28	462	81.6	109	2 S31978	Ig kappa chain - h
29	462	81.6	117	2 S46371	Ig kappa chain V-J

30 461.5 81.5 124 2 S40336 Ig kappa chain V-J
31 461 81.4 107 2 JLO139 Ig kappa chain V r
32 461 81.4 108 1 K1HUOU Ig kappa chain V-I
33 461 81.4 125 2 S40333 Ig kappa chain V-J
34 459 81.1 108 1 K1HUDE Ig kappa chain V-I
35 459 81.1 125 2 S40350 Ig kappa chain - h
36 459 81.1 129 2 S40369 Ig kappa chain - h
37 459 81.1 131 2 S40352 Ig kappa chain V-J
38 458 80.9 107 2 S3262 Ig lambda chain V
39 455 80.4 109 2 S31983 Ig kappa chain - h
40 455 80.4 117 2 S46376 Ig kappa chain V-J
41 454.5 80.3 108 2 S30521 Ig kappa chain V r
42 453 80.0 109 2 S32001 Ig kappa chain - h
43 452 79.9 128 2 S46372 Ig kappa chain var
44 452 79.9 129 2 S52789 Ig kappa chain V r
45 450.5 79.6 108 2 S34007 Ig kappa chain V r

ALIGNMENTS

RESULT 1
S40331
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 511; DB 2; Length 123;
Best Local Similarity 92.7%; Pred. No. 11e-35;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLIYGASSLQSGVPS 60
Db 17 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLIYGASSLQSGVPS 76
Qy 61 RFGSGSGTDTLTITISLQPEDFATYVCROSYSTPPSCSFQGTKEIK 109
Db 77 RFGSGSGTDTLTITISLQPEDFATYVCROSYSTPPR--TFGQGTKEIK 123

RESULT 2
S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 509; DB 2; Length 127;

Best Local Similarity 91.7%; Pred. No. 1.6e-35;
Matches 100; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 18 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVPS 77

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICRQSYSTPPECSFGQGTKEIK 109
Db 78 RFSGSGSGTDFTLTISLQPEDFATYICQSYSTP--WTFGGTKVEIK 124

RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:P:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 505; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 2.9e-35;
Matches 100; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICRQSYSTPPECSFGQGTKEIK 109
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICQSYSTP--LTFGGTKVEIK 107

RESULT 4
S46370
Ig kappa chain V-J region (T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46370; S38644
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46370
A:Molecule type: mRNA
A:Residues: 1-120 <BEN>
A:Cross-references: EMBL:227171; NID:9415957; PID:CAA81695.1; PID:9415958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 88.7%; Score 502; DB 2; Length 120;
Best Local Similarity 88.9%; Pred. No. 5.7e-35;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 11 DIQMTQSPSSLSASVGDRTVITCRASRISISFLNWKQKPKAPOLLIVASRLQSGVPS 70

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICRQSYSTPPECSFGQGTKEIK 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICRQSYSTPPECSFGQGTKEIK 108

Db 71 RFSGSGSGTDFTLTISLQPEDFATYICQSFNSNPPEVTFQGTKEIK 118

RESULT 5
S40317
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40317
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40317
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72427; NID:9441322; PID:CAA51095.1; PID:9441323
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 500; DB 2; Length 129;
Best Local Similarity 89.0%; Pred. No. 9e-35;
Matches 97; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 22 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 81

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICRQSYSTPPECSFGQGTKEIK 109
Db 82 RFSGSGSGTDFTLTISLQPEDFATYICQSYSTP--TFGGTKVEIK 128

RESULT 6
K1HWK
Ig kappa chain precursor V-I region (Walker) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01883
R:Klobeck, H.G.; Combratio, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines
A:Reference number: A93534; MUID:85014148; PMID:6091049
A:Accession: A01883
A:Molecule type: DNA
A:Residues: 1-129 <KLO>
A:Cross-references: UNIPROT:P04431
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two heavy (lambda) chains. In some cases, such as IGA and IGM, the subunits associate into a hexamer.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-123/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>
F:23-45/Region: framework 1
F:38-112/Domain: immunoglobulin homology <IMM>
F:46-56/Region: complementarity-determining 1
F:57-71/Region: framework 2
F:72-78/Region: complementarity-determining 2
F:79-110/Region: framework 3
F:111-119/Region: complementarity-determining 3
F:120-129/Region: framework 4
F:45-110/Disulfide bonds: #status predicted

Query Match 86.7%; Score 491; DB 1; Length 129;
Best Local Similarity 90.8%; Pred. No. 5e-34;
Matches 99; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

```
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 23 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVTS 82
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSPPPCSFQGGTKLEIK 109
Db 83 RFSGSGSGTDFTLTISSLQPEDSATYYCQOSYST--LITFGQGRLEIK 129

RESULT 7
S44122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44122
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Status: preliminary
A;Accession: S44122
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 489; DB 2; Length 108;
Best Local Similarity 83.9%; Pred. No. 6.2e-34; Mismatches 5; Indels 2; Gaps 1;
Matches 98; Conservative 4;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSPPPCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFAIYYCQOSYSTP--WTFGQGRKVEIK 107

RESULT 8
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MC1>
A;Cross-references: EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID:g506423
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 489; DB 2; Length 108;
Best Local Similarity 88.1%; Pred. No. 6.2e-34; Mismatches 7; Indels 2; Gaps 1;
Matches 96; Conservative 7;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 ETELQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSPPPCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQOSYSTP--ITSGQGRLEIK 107
```

```
RESULT 9
K1HUHU
Ig kappa chain V-I region (Hau) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A01868; S02574
R;Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A;Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg;
A;Reference number: A01868; MUID:71032830; PMID:4097974
A;Accession: A01868
A;Molecule type: protein
A;Residues: 1-108 <WAT>
A;Cross-references: UNIPROT:P01600
A;Note: the C region of this chain has the Inv (3) marker
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the;
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 85.7%; Score 485; DB 1; Length 108;
Best Local Similarity 87.2%; Pred. No. 1.3e-33; Mismatches 4; Indels 2; Gaps 1;
Matches 95; Conservative 8;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPQVLLIYAASSLPSCGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSPPPCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITP--TSFGQGRVEIK 107

RESULT 10
S31981
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31981
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31981
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <FOR>
A;Cross-references: EMBL:Z15077; NID:g38493; PIDN:CAA78786.1; PID:g38494
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 484; DB 2; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33; Mismatches 5; Indels 2; Gaps 1;
Matches 94; Conservative 8;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 ELVMTQSPSSLSASVGRVTITCRASQDISRYLNWYQKPGKAPKLLIHGASTLESQVPG 60
```

```
Qy 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTPECSFGQGTKEIK 109
|||||
Db 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTP--FTFGQGTKEIK 107

RESULT 11
S31998
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31998
R:Portolano, S.; Chazebalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31998
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15081; NID:g38501; PIDN:CAA78790.1; PID:g38502
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 482; DB 2; Length 109;
Best Local Similarity 87.2%; Pred. No. 2.4e-33;
Matches 95; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
:: |||||
Db 1 ELVMTQSPSSLSASVGDRTVITCRASQISAYLNWYQKPKAPKLLIYSASSLSQSGVPS 60

Qy 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTPECSFGQGTKEIK 109
|||||
Db 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTP--WTFHGQGTKEIK 107

RESULT 12
S40314
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40314
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40314
A>Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <KLE>
A:Cross-references: EMBL:X72424
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 482; DB 2; Length 122;
Best Local Similarity 86.2%; Pred. No. 2.6e-33;
Matches 94; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
|||||
Db 16 DIQMTQSPSSLSASVGDRTVITCRASQISNNYLNWYQKPKAPNLLISAASSLSQSGVPS 75

Qy 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTPECSFGQGTKEIK 109
|||||
Db 76 RFSGSGGTDFLTITSSIQPEDFGTYCQYTHTPP--FTFGQGTKEIK 122

RESULT 13
S36275
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C:Species: Homo sapiens (man)
```

```
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36275
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36275
A>Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID:g939909
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 480.5; DB 2; Length 107;
Best Local Similarity 87.2%; Pred. No. 3.1e-33;
Matches 95; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLAWYQKPKGVKPLLIYAASTLSQSGVPS 60

Qy 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTPECSFGQGTKEIK 109
|||||
Db 61 RFSGSGGTDFLTITSSIQPEDVAVYCCQYISTP---TFGQGTKEIK 106

RESULT 14
S52793
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S52793
R:Rocca, A.; Khamilichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma
A:Reference number: S52789
A:Accession: S52793
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85997; NID:g758600; PIDN:CAAS9989.1; PID:g758601
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 476; DB 2; Length 129;
Best Local Similarity 85.3%; Pred. No. 8.8e-33;
Matches 93; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
|||||
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQNIISYLNWYQKPKAPKLLIYAAASSLSQSGVPA 82

Qy 61 RFSGSGGTDFLTITSSIQPEDFATYYCQSYSTPECSFGQGTKEIK 109
|||||
Db 83 RFVSGSGGTDFLTITSSIQPEDFATYYCQYISAP--LTFGGGTKEIK 129

RESULT 15
S24206
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S24206; S24209
R:Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regi
A:Reference number: S24205; MUID:91330953; PMID:1907917
A:Accession: S24206
A:Molecule type: DNA
A:Residues: 1-117 <PAR>
```


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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 61.1121 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-10

Perfect score: 566

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPSCSFGQGTKEIK 109

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	497.5	87.9	107	2	Q96SA9
2	496	87.6	108	2	Q9UL77
3	491	86.7	129	1	KV1W_HUMAN
4	485	85.7	108	1	KV1H_HUMAN
5	475.5	84.0	107	2	Q9UL81
6	473	83.6	236	2	Q6GMW1
7	471	83.2	236	2	Q6GMX0
8	467	82.5	236	2	Q6GMX8
9	465	82.2	236	2	Q7Z3Y4
10	461	81.4	108	1	KV1N_HUMAN
11	461	81.4	236	2	Q6PIH7
12	460	81.3	108	2	Q9UL70
13	459	81.1	108	1	KV1E_HUMAN
14	450	79.5	108	1	KV1M_HUMAN
15	449.5	79.4	109	1	KV1T_HUMAN
16	449	79.3	108	1	KV1R_HUMAN
17	449	79.3	108	2	Q9UL79
18	448	79.2	108	1	KV1G_HUMAN
19	446	78.8	108	1	KV1Y_HUMAN
20	444	78.4	108	1	KV1O_HUMAN
21	442	78.1	108	1	KV1B_HUMAN
22	442	78.1	108	1	KV1V_HUMAN
23	441	77.9	108	1	KV1S_HUMAN
24	440	77.7	108	1	KV1F_HUMAN
25	437	77.2	108	1	KV1A_HUMAN
26	437	77.2	244	2	Q6SZC8
27	435	76.9	234	2	Q7Z473
28	435	76.9	236	2	Q6PIH4
29	434	76.7	108	1	KV1K_HUMAN
30	434	76.7	236	2	Q6GMX9
31	433	76.5	108	1	KV1P_HUMAN

32	432	76.3	240	2	Q65ZC9
33	431.5	76.2	107	1	KV1D_HUMAN
34	430	76.0	108	1	KV1Q_HUMAN
35	427	75.4	108	1	KV1C_HUMAN
36	427	75.4	129	1	KV1X_HUMAN
37	427	75.4	236	2	Q6PI75
38	425	75.1	108	1	KV1L_HUMAN
39	425	75.1	117	1	KV1J_HUMAN
40	417	73.7	117	1	KV1I_HUMAN
41	407	71.9	116	2	Q96PF6
42	403	71.2	108	1	KV5M_MOUSE
43	403	71.2	114	1	KV4A_HUMAN
44	399	70.5	108	1	KV5J_MOUSE
45	397	70.1	109	2	Q920E6

Q65ZC9 homo sapien
P01596 homo sapien
P01609 homo sapien
P01595 homo sapien
P04432 homo sapien
Q6PI75 homo sapien
P01604 homo sapien
P01601 homo sapien
Q96PF6 homo sapien
P01646 mus musculu
P01625 homo sapien
P01643 mus musculu
Q920E6 mus musculu

ALIGNMENTS

RESULT 1
Q96SA9 ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Addeerson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; .
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; IBMW
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 87.9%; Score 497.5; DB 2; Length 107;
Best Local Similarity 90.8%; Pred. No. 8.2e-42;
Matches 99; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYAASSLSQGVPS	60
Qy	61	RFGSGSGTFTLTISLQPEDFATYTCROSYSPTPPSCSFGQGTKEIK	109
Db	61	RFGSGSGTFTLTISLQPEDFATYTCROSYSPTPPSCSFGQGTKEIK	106

RESULT 2
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;

```
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AAD56273.1; -;
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
SQ
Query Match 87.6%; Score 496; DB 2; Length 108;
Best Local Similarity 89.9%; Pred. No. 1.2e-41;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSQSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSQST--SWTFEGGTYKVEIK 107
RESULT 3
KV1W HUMAN
ID_KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014148; PubMed=6091049;
RA Klobeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006 (1984).
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HWUK.
DR HSSP; P01607; 1BWW.
```

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129
FT SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;
SQ
Query Match 86.7%; Score 491; DB 1; Length 129;
Best Local Similarity 90.8%; Pred. No. 4.5e-41;
Matches 99; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 23 DIQWTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVTS 82
Qy 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSQSTPPSCSFQGGTKLEIK 109
Db 83 RFSGSGSGDTFTLTISLQPEDSATYYCQSQSYST--LITFGQGRLEIK 129
RESULT 4
KV1H HUMAN
ID_KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1HWU.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
```

FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 85.7%; Score 485; DB 1; Length 108;
 Best Local Similarity 87.2%; Pred. No. 1.5e-40;
 Matches 95; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
 Db 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPQVLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLOPEDFATYICROSYPPECSFGQGTKEIK 109
 Db 61 RFGSGSGTDFTLTISSLOPEDFATYICQNYITP--TSFGQGTKEIK 107

RESULT 5
 Q9UL81 PRELIMINARY; PRT; 107 AA..

AC Q9UL81
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035033; AAD56269.1; -.
 DR HSSP; P01607; 1BWW.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 84.08; Score 475.5; DB 2; Length 107;
 Best Local Similarity 86.2%; Pred. No. 1.3e-39;
 Matches 94; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
 Db 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPNLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLOPEDFATYICROSYPPECSFGQGTKEIK 109
 Db 61 RFGSGSGTDFTLTISSLOPEDFATYICQSYSA--LTFGPGTKVDIR 106

RESULT 6
 Q6GMW1 PRELIMINARY; PRT; 236 AA.

AC Q6GMW1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Casavant T.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL; BC073791; AAH73791.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein_MHC;
 SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFAC437 CRC64;

Query Match 83.6%; Score 473; DB 2; Length 236;
 Best Local Similarity 88.0%; Pred. No. 5.6e-39;
 Matches 95; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 2 IQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPSR 61
 Db 24 IQWQSPSSLSASVGRVITTCRASQISNDLQWYQKPGKAPKLLIYAASSLSQGVPSR 83

Qy 62 FSGSGSGTDFTLTISSLOPEDFATYICROSYPPECSFGQGTKEIK 109
 Db 84 FSGSGSGTDFTLTISSLOPEDFATYICLDYNYP--WTFQGTKEIK 129

RESULT 7
 Q6GMX0 PRELIMINARY; PRT; 236 AA.

AC Q6GMX0
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
DR HSSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFB4ED23084BC6 CRC64;

Query Match 82.2%; Score 465; DB 2; Length 236;
Best Local Similarity 86.2%; Pred. No. 3.5e-38;
Matches 94; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQSGVPS 60
Db 23 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQSGVPS 82
Qy 61 RFSGSGSGTDTLTITSSLPQDFATYTCROSYSPTPPECSPGQGTLEIK 109
Db 83 KFGSGSGTDTLTITSSLPQDFATYTCQYKSP--VTFGQGTLEIK 129

RESULT 10
KV1N HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59 (1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
DR PIR; A01872; KIHOUU.
DR HSSP; P01607; 1BWV.

DR GO; GO:0005756; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 23 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 81.4%; Score 461; DB 1; Length 108;
Best Local Similarity 75.2%; Pred. No. 3.6e-38;
Matches 82; Conservative 18; Mismatches 7; Indels 2; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQSGVPS 60
Qy 61 RFSGSGSGTDTLTITSSLPQDFATYTCROSYSPTPPECSPGQGTLEIK 109
Db 61 RFSGSGSGTDTLTITSSLPQDFATYTCZSYSP--TTFGQGTLEIK 107

RESULT 11
Q6PIH7 PRELIMINARY; PRT; 236 AA.
ID Q6PIH7
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Lung.
RC SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
```

Query Match 81.4%; Score 461; DB 2; Length 236;
Best Local Similarity 83.5%; Pred. No. 8.8e-38;
Matches 91; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 23 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPKAPKLLIYGASSLSQGVPS 82

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYCRQSYSTPPECSEFGQGTKEIK 109

Db 83 RFSGSGSGTEFTLTISSLQPEDFATYCRQSYSTPPECSEFGQGTKEIK 129

RESULT 12

```
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
```

Query Match 81.3%; Score 460; DB 2; Length 108;
Best Local Similarity 85.3%; Pred. No. 4.5e-38;
Matches 93; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPKAPKLLIYGASSLSQGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYCRQSYSTPPECSEFGQGTKEIK 109

Db 61 RFSGSGSGTDFTLTISSLQPEDFATYCRQSYSTPPECSEFGQGTKEIK 107

RESULT 13

```
KVIE_HUMAN
ID KVIE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P.; Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR PIR; A01865; K1HUDE.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;
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Query Match 81.1%; Score 459; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 5.6e-38;
Matches 87; Conservative 12; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISINLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 1 BIZMTQSPSSLSASVGRVTITCRASQSVNKLWYQKPKAPKLLIYFAASSLSKGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYCRQSYSTPPECSEFGQGTKEIK 108

Db 61 RFSGSGSGTDFTLTISGLLPEDFATYCRQSYSTPPECSEFGQGTKEIK 106

RESULT 14

```
KVIM_HUMAN
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D.; Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
```

RT anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: The second and third hypervariable regions of this
CC chain are identical with those of the human POM V-III kappa chain,
CC with which it shares certain idiotypic determinants.
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
CC PIR; A01871; KIHULY.
DR HSP; P01607; LEW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 79.5%; Score 450; DB 1; Length 108;
Best Local Similarity 78.9%; Pred. No. 4.4e-37;
Matches 86; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQSNVAYLNWYQKPKAPKLLIYGASTREAGVPS 60

Qy 61 RFGSGSGTDTFTLTISLQPEDFATYYCROSYSYTPPECSPGQGTKEIK 109
Db 61 RFGSGSGTDTFTLTISLQPEDIATYYCQVNNWPP--TFGQGTKEVVK 107

RESULT 15
KVIT HUMAN
ID -KVIT HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Mev.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic Bence-
RT Jones Protein (Mev). An unusual insertion in the third hypervariable
RT region of a human kappa-immunoglobulin light chain."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC -I- MISCELLANEOUS: Another form that lacked residues 1-3 was also
CC found.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC PIR; A01879; KIHUMV.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 98 Complementarity-determining-3.
FT DOMAIN 99 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11870 MW; B6ABF4515D55F5A0 CRC64;

Query Match 79.4%; Score 449.5; DB 1; Length 109;
Best Local Similarity 80.7%; Pred. No. 5e-37;
Matches 88; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 1 DVQWTQSPSSLSASVGDRTVITCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQGVPS 60

Qy 61 RFGSGSGTDTFTLTISLQPEDFATYYCROSYSYTPPECSPGQGTKEIK 109
Db 61 RFGSGSGTDTFTLTISLQDDFATYYCQOSY--TNPEVTFGGTVDIK 108

Search completed: November 16, 2005, 22:01:51
Job time : 62.1121 secs

CONFIDENTIAL

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.534 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357a-10
Perfect score: 566
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYTPPECSFGQGTKLEIK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	90.3	240	4	US-09-192-854-2
2	505.5	89.3	108	3	US-09-240-274-32
3	505.5	89.3	108	3	US-09-240-274-43
4	505	89.2	108	2	US-08-379-057-29
5	504	89.0	108	3	US-09-025-769B-14
6	504	89.0	108	4	US-09-490-070A-14
7	504	89.0	108	4	US-09-490-153-14
8	504	89.0	108	4	US-09-490-324-14
9	501.5	88.6	108	3	US-09-240-274-167
10	500	88.3	109	3	US-09-025-769B-28
11	500	88.3	109	3	US-09-025-769B-43
12	500	88.3	109	4	US-09-490-070A-28
13	500	88.3	109	4	US-09-490-070A-43
14	500	88.3	109	4	US-09-490-153-28
15	500	88.3	109	4	US-09-490-153-43
16	500	88.3	109	4	US-09-490-324-28
17	500	88.3	109	4	US-09-490-324-43
18	499	88.2	107	1	US-08-276-852-105
19	499	88.2	107	1	US-08-899-575-105
20	499	88.2	107	1	US-08-899-575-105
21	499	88.2	107	5	PCT-US95-08743-105
22	498	88.0	107	1	US-08-276-852-104
23	498	88.0	107	1	US-08-899-575-104
24	498	88.0	107	1	US-08-899-575-104
25	498	88.0	107	5	PCT-US95-08743-104
26	497	87.8	107	3	US-09-240-274-158
27	496.5	87.7	108	1	US-08-276-852-109

28	496.5	87.7	108	1	US-08-899-575-109	Sequence 109, App
29	496.5	87.7	108	1	US-08-899-575-109	Sequence 109, App
30	496.5	87.7	108	5	PCT-US95-08743-109	Sequence 109, App
31	496	87.6	107	3	US-09-240-274-37	Sequence 37, Appl
32	495.5	87.5	108	3	US-09-240-274-41	Sequence 41, Appl
33	494	87.3	107	3	US-09-240-274-156	Sequence 156, App
34	494	87.3	107	3	US-09-240-274-175	Sequence 175, App
35	494	87.3	107	3	US-09-240-274-176	Sequence 176, App
36	492	86.9	107	3	US-09-240-274-44	Sequence 44, Appl
37	492	86.9	107	3	US-09-240-274-168	Sequence 168, App
38	491.5	86.8	108	3	US-09-240-274-181	Sequence 181, App
39	491.5	86.8	114	2	US-08-561-521-43	Sequence 43, Appl
40	491.5	86.8	114	5	PCT-US95-01219-43	Sequence 43, Appl
41	491	86.7	107	2	US-08-652-558-36	Sequence 36, Appl
42	491	86.7	107	2	US-08-378-939-14	Sequence 14, Appl
43	491	86.7	214	4	US-09-472-087-71	Sequence 71, Appl
44	488	86.2	107	3	US-09-240-274-38	Sequence 38, Appl
45	488	86.2	107	3	US-09-240-274-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 240
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match	90.3%	Score 511;	DB 4;	Length 240;
Best Local Similarity	92.7%	Pred. No. 2.4e-39;		
Matches 101;	Conservative 4;	Mismatches 2;	Indels 2;	Gaps 1;
Qy	1	DIQMTQSPSSLSASVGRVTITCRASQISINYNLWYQKQKAPKLLIYGCASSLSQSGVPS	60	
Db	133	DIQMTQSPSSLSASVGRVTITCRASQISINYNLWYQKQKAPKLLIYGCASSLSQSGVPS	192	
Qy	61	RFGSGSGTDTLTITSSLPQEDFATYVCROSYSTPPECSEFGQGTKLEIK	109	
Db	193	RFGSGSGTDTLTITSSLPQEDFATYVCROSYSTPPECSEFGQGTKLEIK	239	
RESULT 2				
US-09-240-274-32				
; Sequence 32, Application US/09240274				
; Patent No. 6255455				
; GENERAL INFORMATION:				
; APPLICANT: Siegel, Donald L.				
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL				
; FILE REFERENCE: 09596-4202				
; CURRENT APPLICATION NUMBER: US/09/240,274				
; CURRENT FILING DATE: 1999-01-29				
; EARLIER APPLICATION NUMBER: 60/081,380				
; EARLIER FILING DATE: 1998-04-10				
; EARLIER APPLICATION NUMBER: 60/028,550				
; NUMBER OF SEQ ID NOS: 224				

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match      89.3%; Score 505.5; DB 3; Length 108;
Best Local Similarity 92.5%; Pred. No. 3.2e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 3 QMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPSRF 62
Db 2 ELTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

Qy 63 SGSGSGTDTLTITSLQPEDFATYCYQSYSTPPSCSFQGTGLEIK 109
Db 62 SGSGSGTDTLTITSLQPEDFATYCYQSYSTPP-YTFGQGTGLEIK 107

RESULT 3
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      89.3%; Score 505.5; DB 3; Length 108;
Best Local Similarity 92.5%; Pred. No. 3.2e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 3 QMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPSRF 62
Db 2 ELTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

Qy 63 SGSGSGTDTLTITSLQPEDFATYCYQSYSTPPSCSFQGTGLEIK 109
Db 62 SGSGSGTDTLTITSLQPEDFATYCYQSYSTPP-YTFGQGTGLEIK 107

RESULT 4
US-08-379-057-29
; Sequence 29, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jorgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; OTHER INFORMATION: Different Epitopes of Human gp39 and Methods For Their Use
```

```
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-29

Query Match      89.2%; Score 505; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 3.6e-39;
Matches 100; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGTDTLTITSLQPEDFATYCYQSYSTPPSCSFQGTGLEIK 109
Db 61 RFSGSGSGTDTLTITSLQPEDFATYCYQSYSTP--LTFGGKTKEIK 107

RESULT 5
US-09-025-769B-14
; Sequence 14, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9090
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-025-769B-14

Query Match      89.0%; Score 504; DB 3; Length 108;
Best Local Similarity 91.7%; Pred. No. 4.4e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCROSYSTPECSFGQGTKEIK 109
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCQYYSTP--LTFGGGTKVEIK 107

RESULT 6
US-09-490-070A-14
; Sequence 14, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
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/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-070A-14

Query Match      89.0%; Score 504; DB 4; Length 108;
Best Local Similarity 91.7%; Pred. No. 4.4e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCROSYSTPECSFGQGTKEIK 109
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCQYYSTP--LTFGGGTKVEIK 107

RESULT 7
US-09-490-153-14
; Sequence 14, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-153-14
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Query Match 89.0%; Score 504; DB 4; Length 108;
 Best Local Similarity 91.7%; Pred. NO. 4.4e-39;
 Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWTSPLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYGASSLQSGVPS 60
 Db 1 DIQWTSPLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYAASSLQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 109
 Db 61 RFGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 107

RESULT 8
 US-09-490-324-14
 ; Sequence 14, Application US/09490324
 ; Patent No. 6828422
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,324
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769
 ; FILING DATE: 18-FEB-1998
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-490-324-14

Query Match 89.0%; Score 504; DB 4; Length 108;
 Best Local Similarity 91.7%; Pred. NO. 4.4e-39;
 Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWTSPLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYGASSLQSGVPS 60
 Db 1 DIQWTSPLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYAASSLQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 109
 Db 61 RFGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 107

Db 61 RFGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 107

RESULT 9
 US-09-240-274-167
 ; Sequence 167, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ; FILE REFERENCE: 09596-4202
 ; CURRENT APPLICATION NUMBER: US/09/240,274
 ; CURRENT FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 167
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
 US-09-240-274-167

Query Match 88.6%; Score 501.5; DB 3; Length 108;
 Best Local Similarity 91.6%; Pred. NO. 7.5e-39;
 Matches 98; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Qy 3 QMTQSPSSLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYGASSLQSGVPSRF 62
 Db 2 ELTQSPSSLSASVGDVVTITCRASQISINLWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 63 SGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 109
 Db 62 SGSGSGTDFTLTISSLPEDFATYYCQYSYTP--LTFGGGKVEIK 107

RESULT 10
 US-09-025-769B-28
 ; Sequence 28, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:

```
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-28

Query Match      88.3%; Score 500; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYVCROSYSTPPSCSFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLPEDFATYVCQOHTTTP--TFGQGTKEIK 107

RESULT 11
US-09-025-769B-43
; Sequence 43, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-43
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Query Match      88.3%; Score 500; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYVCROSYSTPPSCSFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLPEDFATYVCQOHTTTP--TFGQGTKEIK 107

RESULT 12
US-09-490-070A-28
; Sequence 28, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
; US-09-490-070A-28

Query Match      88.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYVCROSYSTPPSCSFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLPEDFATYVCQOHTTTP--TFGQGTKEIK 107
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Db 61 RFGSGSGTDTLTITSSLPEDFATYYCQHYHTTP--TFQGTKEIK 107

RESULT 13

US-09-490-070A-43
; Sequence 43, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-490-070A-43

Query Match 88.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGRVTITCRASQISNLYNMWQKPGKAPKLLIYGASSLSQSGVPS 60

Db 1 DIQMTSPSSLSASVGRVTITCRASQISNLYNMWQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPEDFATYYCQHYHTTP--TFQGTKEIK 109

Db 61 RFGSGSGTDTLTITSSLPEDFATYYCQHYHTTP--TFQGTKEIK 107

RESULT 14

US-09-490-153-28
; Sequence 28, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

; Moroney, Simon
; Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-490-153-28

Query Match 88.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGRVTITCRASQISNLYNMWQKPGKAPKLLIYGASSLSQSGVPS 60

Db 1 DIQMTSPSSLSASVGRVTITCRASQISNLYNMWQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTITSSLPEDFATYYCQHYHTTP--TFQGTKEIK 109

Db 61 RFGSGSGTDTLTITSSLPEDFATYYCQHYHTTP--TFQGTKEIK 107

RESULT 15

US-09-490-153-43
; Sequence 43, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/490,153
;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 596-9000
;; TELEFAX: (212) 596-9090
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 109 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-490-153-43

Query Match 80.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQHHYTPP--TFGQGTKEIK 107

Search completed: November 16, 2005, 22:07:18
Job time : 18.534 secs

10/20/2011 10:10:10 AM

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 66.9228 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-10

Perfect score: 566

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPECSTFGQTKLEIK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	566	100.0	109	14	US-10-330-613-10
2	566	100.0	109	14	US-10-330-530-10
3	566	100.0	109	16	US-10-660-357-10
4	520	91.9	108	17	US-10-726-332-214
5	520	91.9	108	17	US-10-805-177-64
6	519	91.7	108	17	US-10-726-332-18
7	517	91.3	108	17	US-10-726-332-28
8	512	90.5	107	17	US-10-727-155-308
9	512	90.5	108	17	US-10-726-332-209
10	511	90.5	238	20	US-11-031-485-28
11	511	90.3	107	10	US-09-791-153A-67

12	511	90.3	108	16	US-10-409-814A-4	Sequence 4, Appli
13	511	90.3	108	17	US-10-805-177-20	Sequence 20, Appli
14	511	90.3	240	9	US-09-192-854-2	Sequence 2, Appli
15	511	90.3	240	9	US-09-968-561A-2	Sequence 2, Appli
16	511	90.3	240	10	US-09-968-744A-2	Sequence 2, Appli
17	511	90.3	240	11	US-09-968-561A-2	Sequence 2, Appli
18	511	90.3	240	16	US-10-744-774-1	Sequence 1, Appli
19	511	90.3	240	20	US-11-115-682-2	Sequence 22, Appli
20	509	89.9	108	17	US-10-726-332-22	Sequence 220, App
21	508.5	89.8	111	17	US-10-726-332-22	Sequence 100, App
22	508	89.8	111	18	US-10-916-840-100	Sequence 124, App
23	505.5	89.3	107	20	US-11-031-485-124	Sequence 32, Appli
24	505.5	89.3	108	10	US-09-848-798-32	Sequence 43, Appli
25	505.5	89.3	108	10	US-09-848-798-43	Sequence 221, App
26	505.5	89.3	111	17	US-10-726-332-221	Sequence 128, App
27	505	89.2	106	20	US-11-031-485-128	Sequence 56, Appli
28	505	89.2	111	14	US-10-203-754A-56	Sequence 15, Appli
29	504	89.0	108	16	US-10-744-774-15	Sequence 198, App
30	504	89.0	116	17	US-10-783-311-138	Sequence 88, Appli
31	502	88.7	107	15	US-10-309-762-88	Sequence 103, App
32	502	88.7	107	17	US-10-938-353-103	Sequence 167, App
33	501.5	88.6	108	10	US-09-848-798-167	Sequence 5, Appli
34	500	88.3	106	15	US-10-377-121-5	Sequence 8, Appli
35	500	88.3	108	14	US-10-125-687-8	Sequence 8, Appli
36	500	88.3	108	18	US-10-996-191-8	Sequence 4, Appli
37	499.5	88.3	107	15	US-10-363-349-4	Sequence 7, Appli
38	499.5	88.3	288	15	US-10-363-349-7	Sequence 105, App
39	499	88.2	107	14	US-10-016-986-105	Sequence 155, App
40	498	88.0	105	15	US-10-309-762-155	Sequence 104, App
41	498	88.0	107	14	US-10-016-986-104	Sequence 67, Appli
42	498	88.0	107	15	US-10-309-762-67	Sequence 68, Appli
43	498	88.0	107	15	US-10-309-762-68	Sequence 79, Appli
44	498	88.0	107	16	US-10-663-244-79	Sequence 10, Appli
45	498	88.0	107	17	US-10-949-135-10	

ALIGNMENTS

RESULT 1
US-10-330-613-10
; Sequence 10, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-10

Query Match 100.0%; Score 566; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.4e-38;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQISNLYNWYQQKFGKAPKLLIYGASSLQSGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCRASQISNLYNWYQQKFGKAPKLLIYGASSLQSGVPS	60
Qy	61	RFSGSGSGTDFTLTISSLQPEDPATYVCQSSTPPECSTFGQTKLEIK	109
Db	61	RFSGSGSGTDFTLTISSLQPEDPATYVCQSSTPPECSTFGQTKLEIK	109

RESULT 2

```

US-10-330-530-10
; Sequence 10, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-10

Query Match      100.0%; Score 566; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.4e-38;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGGTDFLTITSSLPQEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDFLTITSSLPQEDFATYYCRQSYSTPPESFGQGTKEIK 109

RESULT 3
US-10-660-357-10
; Sequence 10, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-10

Query Match      100.0%; Score 566; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.4e-38;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGGTDFLTITSSLPQEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDFLTITSSLPQEDFATYYCRQSYSTPPESFGQGTKEIK 109

RESULT 4
US-10-726-332-214
; Sequence 214, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes

```

```

; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: AGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-214

Query Match      91.9%; Score 520; DB 17; Length 108;
Best Local Similarity 93.6%; Pred. No. 1.2e-34;
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDFLTITSSLPQEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDFLTITSSLPQEDFATYYCQSQSYSTPP--TFQGTKEIK 107

RESULT 5
US-10-805-177-64
; Sequence 64, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-64

Query Match      91.9%; Score 520; DB 17; Length 108;
Best Local Similarity 93.6%; Pred. No. 1.2e-34;
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60

```

Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCCSFQGTKEIK 109
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 6

US-10-726-332-18
; Sequence 18, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao-Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-18

Query Match 91.7%; Score 519; DB 17; Length 108;
Best Local Similarity 93.6%; Pred. No. 1.5e-34;
Matches 102; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 60
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCCSFQGTKEIK 109
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 7

US-10-726-332-28
; Sequence 28, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao-Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-28

Query Match 91.3%; Score 517; DB 17; Length 108;
Best Local Similarity 92.7%; Pred. No. 2.1e-34;
Matches 101; Conservative 5; Mismatches 1; Indels 2; Gaps 1;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 60
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCCSFQGTKEIK 109
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 8

US-10-727-155-308
; Sequence 308, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao-Feng
; APPLICANT: Scott Kiakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-308

Query Match 90.5%; Score 512; DB 17; Length 107;
Best Local Similarity 92.7%; Pred. No. 5.3e-34;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 60
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCCSFQGTKEIK 109
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--ITFGQGTKEIK 107

RESULT 9

US-10-726-332-209
; Sequence 209, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao-Feng

; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX 072A
; CURRENT APPLICATION NUMBER: US/10/726.332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-209

Query Match 90.5%; Score 512; DB 17; Length 108;
Best Local Similarity 92.7%; Pred. No. 5.4e-34;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCROSSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDTLTITSSLPQEDFATYYCQSYSTP--ITFGQGTKEIK 107

RESULT 10
US-11-031-485-28
; Sequence 28, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031.485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-28

Query Match 90.5%; Score 512; DB 20; Length 238;
Best Local Similarity 89.0%; Pred. No. 1.1e-33;
Matches 97; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYGASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGRVTITCRASQITNVLNWKQKPGKAPKLLIYAASSLPRGVPS 82

Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCROSSYSTPPESFGQGTKEIK 109
Db 83 RFSGSGGTDTLTITSSLPQEDFATYYCQSYSTPPESFGQGTKEIK 131

RESULT 11
US-09-791-153A-67
; Sequence 67, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra

; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791.153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-67

Query Match 90.3%; Score 511; DB 10; Length 107;
Best Local Similarity 92.7%; Pred. No. 6.4e-34;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCROSSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDTLTITSSLPQEDFATYYCQSYSTP--WTFGQGTKEIK 107

RESULT 12
US-10-409-814A-4
; Sequence 4, Application US/10409814A
; Publication No. US20040202995A1
; GENERAL INFORMATION:
; APPLICANT: de Wildt, Rudolf
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS
; FILE REFERENCE: 8039/2032
; CURRENT APPLICATION NUMBER: US/10/409.814A
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-814A-4

Query Match 90.3%; Score 511; DB 16; Length 108;
Best Local Similarity 92.7%; Pred. No. 6.4e-34;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCROSSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDTLTITSSLPQEDFATYYCQSYSTP--WTFGQGTKEIK 107

RESULT 13
US-10-805-177-20
; Sequence 20, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi

Query Match 90.3%; Score 511; DB 16; Length 108;
Best Local Similarity 92.7%; Pred. No. 6.4e-34;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNVLNWKQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCROSSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGGTDTLTITSSLPQEDFATYYCQSYSTP--WTFGQGTKEIK 107

; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIN-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR 006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-20

Query Match 90.3%; Score 511; DB 17; Length 108;
Best Local Similarity 91.7%; Pred. No. 6.4e-34;
Matches 100; Conservative 5; Mismatches 2; Indels 2; Gaps 1;
QY 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 60
QY 61 RFGSGSGTDFTLTISSLPQEDFATYYCROSYSYTPPCSFQGGTKLEIK 109
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQSYSTPN--TFQGGTKVEIK 107

RESULT 14

US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1

; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match 90.3%; Score 511; DB 9; Length 240;
Best Local Similarity 92.7%; Pred. No. 1.4e-33;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 133 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 192
QY 61 RFGSGSGTDFTLTISSLPQEDFATYYCROSYSYTPPCSFQGGTKLEIK 109
Db 193 RFGSGSGTDFTLTISSLPQEDFATYYCQSYSTPN--TFQGGTKVEIK 239

RESULT 15

US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1

; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 90.3%; Score 511; DB 9; Length 240;
Best Local Similarity 92.7%; Pred. No. 1.4e-33;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 133 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 192
QY 61 RFGSGSGTDFTLTISSLPQEDFATYYCROSYSYTPPCSFQGGTKLEIK 109
Db 193 RFGSGSGTDFTLTISSLPQEDFATYYCQSYSTPN--TFQGGTKVEIK 239

Search completed: November 16, 2005, 23:05:40
Job time : 66.9228 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555
Sequence: 1 DIQWTSPLSASVGRVT.....CLOHNSYPLTFGGGTVKEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqpl1980s:.*
2: Geneseqpl1990s:.*
3: Geneseqpl2000s:.*
4: Geneseqpl2001s:.*
5: Geneseqpl2002s:.*
6: Geneseqpl2003as:.*
7: Geneseqpl2003bs:.*
8: Geneseqpl2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	7	ADC99785 Anti-huma
2	555	100.0	107	7	ADD05389 Anti-MUC1
3	555	100.0	107	7	ADF09827 Human ant
4	555	100.0	107	7	ADK18843 Anti-huma
5	555	100.0	107	7	ADK18861 Anti-huma
6	555	100.0	107	7	ADK18594 Anti-huma
7	555	100.0	107	7	ADK18809 Anti-huma
8	555	100.0	107	7	ADP03911 Murine-ex
9	555	100.0	107	8	ADL25406 Human mAb
10	555	100.0	107	8	ADP23399 Human ant
11	555	100.0	107	8	ADP22314 Human ant
12	555	100.0	107	8	ADP22367 Human ant
13	555	100.0	107	8	ADP22302 Human ant
14	552	99.5	107	8	ADP22098 Human ant
15	552	99.5	107	8	ADP22122 Human ant
16	551	99.3	107	7	ADK18590 Anti-huma
17	551	99.3	107	7	ADK18839 Anti-huma
18	551	99.3	107	7	ADK18805 Anti-huma
19	551	99.3	107	8	ADL25398 Human mAb
20	551	99.3	107	8	ADP22318 Human ant
21	548	98.7	107	7	ADP03917 Murine-ex
22	548	98.7	107	8	ADP22102 Human ant
23	547	98.6	107	8	ADP22106 Human ant
24	546	98.4	107	8	ADP22220 Human ant
25	546	98.4	107	8	ADP22126 Human ant

26	544	98.0	107	7	ADP03918	Adp03918 Murine-ex
27	544	98.0	107	8	ADS84418	AdS84418 Human ant
28	544	98.0	107	8	ADR68560	AdR68560 Anti-EPO-
29	544	98.0	234	8	ADS84476	AdS84476 Human ant
30	544	98.0	234	8	ADR68618	AdR68618 Human ant
31	543	97.8	107	8	ADP22350	Adp22350 Human ant
32	543	97.8	110	5	AAU81280	AAU81280 Human trk
33	542	97.7	107	8	ADP22134	Adp22134 Human ant
34	542	97.7	107	8	ADP22138	Adp22138 Human ant
35	542	97.7	107	8	ADP22172	Adp22172 Human ant
36	542	97.7	107	8	ADP22346	Adp22346 Human ant
37	541	97.5	107	7	ADC99789	AdC99789 Anti-huma
38	541	97.5	107	7	ADD05393	AdD05393 Anti-MUC1
39	541	97.5	107	7	ADF09831	AdF09831 Human ant
40	541	97.5	107	7	ADK18842	AdK18842 Anti-huma
41	541	97.5	107	7	ADK18916	AdK18916 Anti-huma
42	541	97.5	107	7	ADK18892	AdK18892 Anti-huma
43	541	97.5	107	7	ADK18612	AdK18612 Anti-huma
44	541	97.5	107	7	ADK18602	AdK18602 Anti-huma
45	541	97.5	107	7	ADK18810	AdK18810 Anti-huma

ALIGNMENTS

RESULT 1

ADC99785
ID ADC99785 standard; protein; 107 AA.

XX AC ADC99785;

XX 01-JAN-2004 (first entry)

DT DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 14.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX Homo sapiens.

XX W02003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; ADC99787.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

XX Claim 3; SEQ ID NO 14; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

CC	light chain protein of the invention.	Best Local Similarity	100.0%;	Pred. No. 9.2e-35;					
XX	Sequence 107 AA;	Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;
XX		Gaps	0;						
Seq									
Query Match									
Best Local Similarity	100.0%;	Score	555;	DB 7;	Length	107;			
Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Db	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Oy	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					
Db	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					
RESULT 2									
ADD05389									
ID	ADD05389	standard;	protein;	107	AA.				
XX									
AC	ADD05389;								
XX									
DT	01-JAN-2004	(first entry)							
XX									
DE	Anti-MUC18	antibody light chain variable region protein, SEQ ID No 14.							
XX									
KW	monoclonal antibody; tumour; MUC18;	proliferation; cytostatic; vaccine;							
KW	antigen; tumour metastasis; melanoma;	metastatic; human; light chain.							
XX									
OS	Homo sapiens.								
XX									
PN	WO2003057006-A2.								
XX									
PD	17-JUL-2003.								
XX									
PF	26-DEC-2002;	2002WO-US041582.							
XX									
PR	28-DEC-2001;	2001US-0346460P.							
XX									
PA	(ABGE-) ABGENIX INC.								
XX									
PI	Gudas J, Bar-Eli M;								
XX									
DR	WPI, 2003-577496/54.								
DR	N-PSDB; ADD05391.								
XX									
PT	Use of monoclonal antibodies against	MUC18	antigen, for diagnosing and						
PT	treating tumors, inhibiting tumor	growth, inhibiting cell invasion							
PT	associated with melanoma, or	increasing survival of an animal	having a						
PT	metastatic tumor.								
XX									
PS	Claim 3; SEQ ID NO 14; 87pp;	English.							
XX									
CC	The invention relates to a novel	monoclonal antibody used for	inhibiting						
CC	tumour growth in an animal. The	tumour inhibition process	comprises						
CC	selecting an animal in need of	treatment for a tumour, providing	a						
CC	monoclonal antibody comprising	a heavy chain amino acid, where	the						
CC	antibody consists of any one of	10 fully defined sequences of	117-123						
CC	amino acids given in the	specification, and where the	monoclonal antibody						
CC	binds MUC18, and contacting	the tumour with the antibody	resulting in						
CC	inhibited proliferation of the	cells. The monoclonal antibody	has						
CC	cytostatic and can be used in	the production of a vaccine. The	monoclonal						
CC	antibodies against the MUC18	antigen are useful for	diagnosing and						
CC	treating tumors, inhibiting	tumour growth (e.g. melanoma,	lung tumour or						
CC	tumour metastasis), inhibiting	cell invasion associated with	melanoma, or						
CC	increasing survival of an	animal having a metastatic	tumour. This						
CC	sequence represents an anti-	MUC18 antibody light chain,	variable region,						
CC	protein of the invention.								
XX									
Seq	Sequence 107 AA;								
Query Match									
Best Local Similarity	100.0%;	Score	555;	DB 7;	Length	107;			
Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Db	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Oy	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					
Db	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					
RESULT 3									
ADF09827									
ID	ADF09827	standard;	protein;	107	AA.				
XX									
AC	ADF09827;								
XX									
DT	12-FEB-2004	(first entry)							
XX									
DE	Human anti-MUC18	monoclonal antibody light chain #4.							
XX									
KW	cell proliferation inhibition; MUC18	tumour antigen;							
KW	anti-MUC18 monoclonal antibody;	tumour metastasis inhibition; tumour;							
KW	carcinoma; cancer; malignancy;	light chain; human.							
XX									
OS	Homo sapiens.								
XX									
PN	WO2003057837-A2.								
XX									
PD	17-JUL-2003.								
XX									
PF	26-DEC-2002;	2002WO-US041580.							
XX									
PR	28-DEC-2001;	2001US-0346414P.							
XX									
PA	(ABGE-) ABGENIX INC.								
XX									
PI	Gudas J;								
XX									
DR	WPI; 2003-598367/56.								
DR	N-PSDB; ADF09829.								
XX									
PT	Inhibiting cell proliferation	associated with expression of	MUC18	tumor					
PT	antigen, involves incubating	and inhibiting cell by	administering	anti-					
PT	MUC18 monoclonal antibody.								
XX									
PS	Claim 3; SEQ ID NO 14; 83pp;	English.							
XX									
CC	The invention comprises a method	for inhibiting cell proliferation							
CC	associated with expression of	MUC18	tumour antigen. The method						
CC	administering anti-MUC18	monoclonal antibody. The method	of the invention						
CC	is useful for inhibiting cell	(e.g. melanoma or tumour cell)							
CC	proliferation associated with	the expression of MUC18	tumour antigen, the						
CC	method is preferably useful	for inhibiting tumour	metastasis. The method						
CC	is useful for inhibiting cell	proliferation in patients	with tumours,						
CC	carcinomas, cancer and	other malignancies. The	present amino acid						
CC	sequence represents a light	chain from an MUC18	tumour antigen-specific						
CC	monoclonal antibody.								
XX									
Seq	Sequence 107 AA;								
Query Match									
Best Local Similarity	100.0%;	Score	555;	DB 7;	Length	107;			
Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Db	1 DIQMTQSPSSLSASVGRVTITCRASQGI	NDLGWYQKPGKAPKRLIYAASSLSQGVPS	60						
Oy	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					
Db	61 RFSGSGSGTEFTLTISSLQPEDFATYYC	LQHN	SYPLTFGGGTKVEIK	107					

PA (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 18; 255pp; English.
XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX SQ Sequence 107 AA;
XX Query Match 100.0%; Score 555; DB 7; Length 107;
XX Best Local Similarity 100.0%; Pred. No. 9.2e-35;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
Oy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPLTFGGTKVEIK 107
RESULT 7
ADK18809
ID ADK18809 standard; protein; 107 AA.
XX ADK18809;
XX 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody protein related sequence #35.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US0000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 233; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX SQ Sequence 107 AA;
XX Query Match 100.0%; Score 555; DB 7; Length 107;
XX Best Local Similarity 100.0%; Pred. No. 9.2e-35;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
Oy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPLTFGGTKVEIK 107
RESULT 8
ADP03911
ID ADP03911 standard; protein; 107 AA.
XX ADP03911;
XX 29-JUL-2004 (first entry)
XX Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 51.
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytostatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; light chain variable domain.
XX Unidentified.
XX WO2003048328-A2.
XX 12-JUN-2003.
XX 02-DEC-2002; 2002WO-US038550.
XX 03-DEC-2001; 2001US-0337275P.
XX (ABGE-) ABGENIX INC.
XX Gudas J, Foltz I, Handa M, Gallo M;
XX WPI; 2003-523295/49.
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX Claim 3; SEQ ID NO 51; 89pp; English.
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC (light chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPKAPKRLIYAASLSQGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 9

ADL25406

ID ADL25406 standard; protein; 107 AA.

XX AC ADL25406;

XX DT 17-JUN-2004 (first entry)

XX DE Human mAb 1.17 light chain variable region protein SEQ ID NO:16.

XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

XX nephritis; mesangial cell proliferation inhibition;

XX mesangial proliferative glomerulonephritis; nephrotropic;

XX antiinflammatory; dermatological; immunosuppressive; antidiabetic;

XX gene therapy; human; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX WO2004024098-A2.

XX 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

PA (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WU, Lichenstein H;

XX WPI; 2004-269881/25.

DR N-PSDB; ADL25405.

XX Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.

PS Disclosure; SEQ ID NO 16; 115pp; English.

XX The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the

CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;

Best Local Similarity 100.0%; Pred. No. 9.2e-35;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPKAPKRLIYAASLSQGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 10

ADP22399

ID ADP22399 standard; protein; 107 AA.

XX AC ADP22399;

XX DT 09-SEP-2004 (first entry)

XX DE Human anti-TNFA antibody light chain variable region SEQ ID NO:305.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;

XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;

XX antibacterial; antiinflammatory; antipsoriatic; antirheumatic;

XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;

XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;

XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;

XX bladder cancer; lung cancer; glioblastoma; stomach cancer;

XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;

XX prostrate cancer; immuno-mediated inflammatory disease;

XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;

XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;

XX septic shock; cachexia; anorexia; multiple sclerosis.

XX OS Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.

XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic diseases such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.

PS Example 10; SEQ ID NO 305; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22419) or (S4, ADP22424). Also described: (1) assaying
CC (MI) the level of TNFA in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFA in

CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF α induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF α induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC as a TNF α antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNF α
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
 |||
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTISLQPEDFATYICLQHNSYPLTFGGTKVEIK 107
 |||
 Db 61 RFGSGSGTFTLTISLQPEDFATYICLQHNSYPLTFGGTKVEIK 107

RESULT 11

ID ADP22314 standard; protein; 107 AA.

XX ADP22314;

XX 09-SEP-2004 (first entry)

XX Human anti-TNF α antibody light chain variable region SEQ ID NO:220.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNF α ;
 KW anti-TNF α antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNF α antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.

XX W02004050683-A2.

XX 17-JUN-2004.

PD 02-DEC-2003; 2003WO-US038281.

PF 02-DEC-2002; 2002US-0430729P.

PR (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
 PI Manchlencho K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 DR N-PSDB; ADP22313.

XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.

PS Example 10; SEQ ID NO 220; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNF α) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNF α in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNF α in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF α induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF α induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNF α antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNF α
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
 |||
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTISLQPEDFATYICLQHNSYPLTFGGTKVEIK 107
 |||
 Db 61 RFGSGSGTFTLTISLQPEDFATYICLQHNSYPLTFGGTKVEIK 107

RESULT 12

ID ADP22367 standard; protein; 107 AA.

XX ADP22367;

XX 09-SEP-2004 (first entry)

XX Human anti-TNF α antibody light chain variable region SEQ ID NO:273.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNF α ;
 KW anti-TNF α antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;

eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 neuroprotective; vasotropic; antiapoptotic; TNF antagonist;
 TNF induced apoptosis; neoplastic disease; breast cancer;
 bladder cancer; lung cancer; glioblastoma; stomach cancer;
 endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 prostate cancer; immuno-mediated inflammatory disease;
 rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 septic shock; cachexia; anorexia; multiple sclerosis.
 Homo sapiens.
 WO2004050683-A2.
 17-JUN-2004.
 02-DEC-2003; 2003WO-US038281.
 02-DEC-2002; 2002US-0430729P.
 (ABGE-) ABGENIX INC.
 Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 WPI; 2004-480601/45.
 New recombinant human monoclonal antibody that specifically binds to
 Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 arthritis.
 Example 10; SEQ ID NO 273; 213pp; English.
 The present invention describes a human monoclonal antibody (I) that
 specifically binds to tumour necrosis factor-alpha (TNF) and comprises:
 (a) a heavy chain complementarity determining region 1 (CDR1) having the
 two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 and (b) a light chain CDR1 having the two fully defined 11 amino acid
 sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 (M1) the level of TNF in a patient sample, comprising contacting with
 the sample; (2) a composition comprising the antibody and TNF in
 the sample; (3) treating (M2) an animal suffering from a
 fragment and a carrier; (4) inhibiting (M3) TNF induced
 apoptosis in an animal by selecting an animal in need of treatment for
 TNF induced apoptosis by administering the human monoclonal antibody of
 (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 antidiabetic, antinflammatory, antipapillary, antipneumatic, eating-
 disorders, immunomodulator, immunosuppressive, nephrotropic,
 neuroprotective, vasotropic and antiapoptotic activities, and can be used
 as a TNF antagonist. The antibody (I) is useful in the preparation of
 medicament for treating TNF induced apoptosis, neoplastic disease such as
 breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 diseases such as rheumatoid arthritis, glomerulonephritis,
 atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 disease, graft-host reactions, septic shock, cachexia, anorexia, and
 multiple sclerosis. The present sequence represents a human anti-TNF
 antibody light chain variable region, which is used in the
 exemplification of the present invention.
 Query Match
 Best Local Similarity 100.0%; Score 555; DB 8; Length 107;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DIQWTSPLSASVGRVITTCRASQGIKNDLGMVQKPKAPKRIIYAASSLSQSGVPS 60
 Qy 61 RFGSGSGTEFTLTISLQPEDFATYVCLQHSYPLTFGGTKVEIK 107
 Db 61 RFGSGSGTEFTLTISLQPEDFATYVCLQHSYPLTFGGTKVEIK 107
 RESULT 13
 ADP22302
 ID ADP22302 standard; protein; 107 AA.
 AC ADP22302;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFa antibody light chain variable region SEQ ID NO:208.
 XX
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNF; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antinflammatory; antipapillary; antipneumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNF antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX
 DR WPI; 2004-480601/45.
 DR N-PSDB; ADP22301.
 XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 208; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNF) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNF in a patient sample, comprising contacting with
 CC the sample; (2) a composition comprising the antibody and TNF in
 CC the sample; (3) treating (M2) an animal suffering from a
 CC fragment and a carrier; (4) inhibiting (M3) TNF induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antidiabetic, antinflammatory, antipapillary, antipneumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNF antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNF
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 CC
 CC Sequence 107 AA;

CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Oy 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

Db 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

RESULT 14

ADP22098

ID ADP22098 standard; protein; 107 AA.

XX ADP22098;

XX 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody light chain variable region SEQ ID NO:4.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) AGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaawami P, Pigott C, Liang ML, Lee R;

PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.

DR N-PSDB; ADP22097.

XX New recombinant human monoclonal antibody that specifically binds to

PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.

XX Example 10; SEQ ID NO 4; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFA induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 99.5%; Score 552; DB 8; Length 107;

Best Local Similarity 99.1%; Pred. No. 1.6e-34;

Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Oy 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

Db 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

RESULT 15

ADP22122

ID ADP22122 standard; protein; 107 AA.

XX AC ADP22122;

XX 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody light chain variable region SEQ ID NO:28.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;

KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.

DR N-PSDB; ADP22121.

XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor- α , useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.

XX Example 10; SEQ ID NO 28; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor- α (TNF α) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNF α in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNF α in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF α induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNF α induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNF α antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNF α
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 99.5%; Score 552; DB 8; Length 107;
Best Local Similarity 99.1%; Pred. No. 1.6e-34;
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKFKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKFKAPKRLIYAASLSQGVPS 60

Oy 61 RFSGSGSGTFTLTITSSIQPEDPATYTCLOHNSYPLTFGGGKVEIK 107

Db 61 RFSGSGSGTFTLTITSSIQPEDPATYTCLOHNNYPLTFGGGKVEIK 107

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 / Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-14
Perfect score: 555
Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CLQHNSTPLTFGGTKVEIK 107
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	537	96.8	125	2 S40353	Ig kappa chain V-J
2	505	91.0	123	2 S40313	Ig kappa chain V-J
3	504	90.8	108	1 KIHUGL	Ig kappa chain V-I
4	503	90.6	107	2 S36269	Ig lambda chain V
5	501	90.3	108	1 KIHUWE	Ig kappa chain V-I
6	497	89.5	107	2 S36262	Ig lambda chain V
7	494	89.0	117	2 S41809	Ig kappa chain V r
8	493	88.8	108	2 S36279	Ig lambda chain V
9	486	87.6	114	2 S46377	Ig kappa chain V-J
10	484	87.2	125	2 S40349	Ig kappa chain V-J
11	481	86.7	108	2 B49047	Ig kappa chain V r
12	480	86.5	132	2 S40334	Ig kappa chain - h
13	476	85.8	107	2 S36264	Ig lambda chain V
14	475	85.6	108	2 S19674	Ig kappa chain V r
15	475	85.6	125	2 S40333	Ig kappa chain V-J
16	475	85.6	129	2 S40369	Ig kappa chain - h
17	470	84.7	126	2 S40335	Ig kappa chain V-J
18	467	84.1	95	2 S69898	Ig kappa chain V r
19	467	84.1	123	2 S40331	Ig kappa chain - h
20	466	84.0	129	2 S52793	Ig kappa chain V r
21	465	83.8	127	2 S40367	Ig kappa chain V-J
22	464	83.6	108	2 S36277	Ig lambda chain V
23	463	83.4	131	2 S40352	Ig kappa chain V-J
24	462	83.2	125	2 S40316	Ig kappa chain - h
25	461.5	83.2	124	2 S40336	Ig kappa chain V-J
26	461	83.1	105	2 S36266	Ig lambda chain V
27	461	83.1	107	2 I69017	anti-HIV1 envelope
28	460	82.9	129	2 S52789	Ig kappa chain V r
29	459	82.7	129	2 S40317	Ig kappa chain - h

ALIGNMENTS

RESULT 1

S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72463
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 96.8%; Score 537; DB 2; Length 125;
Best Local Similarity 96.3%; Pred. No. 3.4e-39;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGNDLQWYQKPKAPKRLIYAASSLQSGVPS 60
Db 15 DIQMTQSPSSLSASVGDRTVITCRASQIGNDLQWYQKPKAPKRLIYAASSLQSGVPS 74
QY 61 RPSGSGSGTEFTLTISGLQPEDFATYICLQHNSTPLTFGGTKVEIK 107
Db 75 RPSGSGSGTEFTLTISGLQPEDFATYICLQHNSTPLTFGGTKVEIK 121

RESULT 2

S40313
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40313
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40313
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72423; NID:g441314; PIDN:CAAS1091.1; PID:g441315
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 91.0%; Score 505; DB 2; Length 123;

```
Best Local Similarity 91.6%; Pred. No. 1.8e-36;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 60
Db 17 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 76

QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 77 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 123

RESULT 3
K1HUGL
IG kappa chain V-I region (Gal) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01867
R;Leure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A:Title: The primary structure of a monoclonal IGM-immunoglobulin (macroglobulin Gal), I
A:Reference number: A01867; MUID:75059122; PMID:4215718
A:Accession: A01867
A:Molecule type: protein
A:Residues: 1-108 <LAU>
A:Cross-references: UNIPROT:P01599
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This chain was isolated from a Waldenström's macroglobulin.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:I36264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 90.8%; Score 504; DB 1; Length 108;
Best Local Similarity 91.6%; Pred. No. 2e-36;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 60

QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 4
S36269
IG lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36269
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 503; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 2.4e-36;
```

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Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYTSSLQSGVPS 60

QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDFATYYCQQTTFPLTFGGGTKLEIK 107

RESULT 5
K1HUWE
IG kappa chain V-I region (WEA) - human
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01876
R;Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A:Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) wit
A:Reference number: A93964; MUID:83273707; PMID:6410398
A:Accession: A01876
A:Molecule type: protein
A:Residues: 1-108 <GON>
A:Cross-references: UNIPROT:P01610
C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:I36264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 90.3%; Score 501; DB 1; Length 108;
Best Local Similarity 89.7%; Pred. No. 3.5e-36;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMVQKPGTAPKRLIYGATSLQSGVPS 60

QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOYSFPWTFGGGTKVEIK 107

RESULT 6
S36262
IG lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36262
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36262
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18842
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.5%; Score 497; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 7.7e-36;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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```
QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIWVTSPLSASIGDVRVTITCRSQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 60
QY 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEIK 107
Db 61 RFGSGSGTDTLTITSSLOPEDFATYFCQANSLPPTFGGGTKEIK 107

RESULT 7
S41809
IG kappa chain V region A30 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S41809
R:Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zed
Eur. J. Immunol. 23, 2868-2875, 1993
A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A:Reference number: S41809; MUID:94039386; PMID:8223863
A:Accession: S41809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <HUB>
A:Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384
C:Genetics: 19/1
A:Introns: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 494; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 60
Db 23 DIQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 82
QY 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYP 95
Db 83 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYP 117

RESULT 8
S36279
IG lambda chain V region (Clone alpha-THY-23) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36279
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Enbleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36279; MUID:93178448; PMID:7679990
A:Accession: S36279
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <GR1>
A:Cross-references: EMBL:Z18831; NID:G33418; PIDN:CAA79283.1; PID:g939911
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 493; DB 2; Length 108;
Best Local Similarity 88.8%; Pred. No. 1.7e-35;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPS 60
QY 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEIK 107
```

RESULT 9

S46377

IG kappa chain V-J region (T33-17) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S46377; S38650

R:Bensimon, C.; Chaetagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46377

A:Molecule type: mRNA

A:Residues: 1-114 <BEN>

A:Cross-references: EMBL:Z27178; NID:g415971; PIDN:CAA81702.1; PID:g415972

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:22-96/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 486; DB 2; Length 114;

Best Local Similarity 91.4%; Pred. No. 7.1e-35;

Matches 96; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 IQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPSR 61

Db 8 IQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPSR 67

QY 62 FSGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEI 106

Db 68 FSGSGSGTDTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEI 112

RESULT 10

S40349

IG kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S40349

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40349

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 484; DB 2; Length 125;

Best Local Similarity 88.7%; Pred. No. 1.1e-34;

Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 IQWTSPLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPSR 61

Db 19 IQLTQSPSSLSASVGDVRVTITCRASQIRNDLQWYQKPGKAPKRLIYAASLSQGVPSR 78

QY 62 FSGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEIK 107

Db 79 FSGSGSGTDTLTITSSLOPEDFATYCYCLOHNSYPLTFGGGTKEIK 124

RESULT 11

B49047

IG kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B49047

R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 481; DB 2; Length 108;
Best Local Similarity 89.7%; Pred. No. 1.8e-34;
Matches 96; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTSPLSASVGDVRVTITCRASQISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGGKVEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYYCQSYSTPLTFGGGKVEIK 107

RESULT 12
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 480; DB 2; Length 132;
Best Local Similarity 86.0%; Pred. No. 2.7e-34;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
DB 22 DIQWTSPLSASVGDVRVTITCRASQISYLNWYQKPGKAPKRLIYAASSLSQSGVPS 81

QY 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGGKVEIK 107
DB 82 RFGSGSGTEFTLTISLQPEDFATYYCQNSYPTFTGGGKVEIR 128

RESULT 13
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: EMBL:218945; NID:G33426; PIDN:CAA79297.1; PID:G939919
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 476; DB 2; Length 107;
Best Local Similarity 86.0%; Pred. No. 4.8e-34;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
DB 1 EIVLTQSPSLSASVGDVRVTITCRASQISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGGKVEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYYCQSYSTPLTFGGGKVDIK 107

RESULT 14
S19674
Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
R;Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on phage
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19674
A;Molecule type: mRNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:G133386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 475; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 5.9e-34;
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
DB 1 EIVLTQSPSLSASVGDVRVTITCRASQISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGGKVEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYYCQNTSPFLTFGGGKLEIK 107

RESULT 15
S40333

Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72443; NID:G441354; PIDN:CAA51111.1; PID:G441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 475; DB 2; Length 125;
Best Local Similarity 86.9%; Pred. No. 6.7e-34;
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
DB 19 DIQWTSPLSASVGDVRVTITCRASQISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 78

Search completed: November 16, 2005, 22:04:07
Job time : 12.7849 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : -- Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504	90.8	108	1 KV1G_HUMAN	P01599 homo sapien
2	501	90.3	108	1 KV1R_HUMAN	P01610 homo sapien
3	499	89.9	236	2 O6GMW1	O6GMW1 homo sapien
4	475	85.6	236	2 O6GMX8	O6GMX8 homo sapien
5	472	85.0	236	2 O6PIH7	O6PIH7 homo sapien
6	469	84.5	108	2 Q9UL70	Q9UL70 homo sapien
7	469	84.5	236	2 O6GMX9	O6GMX9 homo sapien
8	468	84.3	244	2 O65ZC8	O65ZC8 homo sapien
9	464.5	83.7	107	2 Q96SA9	Q96SA9 homo sapien
10	461	83.1	236	2 O6GMX0	O6GMX0 homo sapien
11	461	83.1	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
12	460	82.9	240	2 O65ZC9	O65ZC9 homo sapien
13	456	82.2	108	1 KV1V_HUMAN	P04430 homo sapien
14	454	81.8	108	2 Q9UL77	Q9UL77 homo sapien
15	452	81.4	108	1 KV1S_HUMAN	P01611 homo sapien
16	446	80.4	108	1 KV1H_HUMAN	P01600 homo sapien
17	445	80.2	108	1 KV1W_HUMAN	P80362 homo sapien
18	444	80.0	129	1 KV1W_HUMAN	P04431 homo sapien
19	441	79.5	108	1 KV1F_HUMAN	P01598 homo sapien
20	438.5	79.0	107	2 Q9UL81	Q9UL81 homo sapien
21	438	78.9	129	1 KV1X_HUMAN	P04432 homo sapien
22	438	78.9	236	2 O6PI75	O6PI75 homo sapien
23	437	78.7	108	1 KV1P_HUMAN	O6PI75 homo sapien
24	434	78.2	108	2 Q9UL79	Q9UL79 homo sapien
25	433	78.0	117	1 KV1D_HUMAN	P01601 homo sapien
26	432.5	77.9	107	1 KV1D_HUMAN	P01596 homo sapien
27	430	77.5	108	1 KV1B_HUMAN	P01594 homo sapien
28	430	77.5	108	1 KV1M_HUMAN	P01605 homo sapien
29	429	77.3	108	1 KV1L_HUMAN	P01604 homo sapien
30	428	77.1	108	1 KV1E_HUMAN	P01597 homo sapien
31	428	77.1	108	1 KV1Q_HUMAN	P01609 homo sapien

32	427	76.9	234	2 Q7Z473	Q7Z473 homo sapien
33	425	76.6	108	1 KV1O_HUMAN	P01607 homo sapien
34	424	76.4	236	2 Q6PIH4	Q6PIH4 homo sapien
35	423	76.2	108	1 KV1C_HUMAN	P01595 homo sapien
36	421	75.9	108	1 KV1N_HUMAN	P01606 homo sapien
37	420	75.7	108	1 KV1K_HUMAN	P01603 homo sapien
38	420	75.7	117	1 KV1J_HUMAN	P01602 homo sapien
39	413	74.4	108	1 KV1A_HUMAN	P01593 homo sapien
40	409	73.7	108	1 KV5S_MOUSE	P01652 mus musculus
41	409	73.7	116	2 Q96PF6	Q96PF6 homo sapien
42	408.5	73.6	109	1 KV1T_HUMAN	P01612 homo sapien
43	406	73.2	108	1 KV5Q_MOUSE	P01650 mus musculus
44	406	73.2	108	1 KV5T_MOUSE	P01653 mus musculus
45	396	71.4	108	1 KV5R_MOUSE	P01651 mus musculus

ALIGNMENTS

RESULT 1
KV1G_HUMAN STANDARD; PRT; 108 AA.
ID KV1G_HUMAN
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=75059122; PubMed=4215718;
RX Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
DR PIR; A01867; KJHUGL.
DR HSSP; P01607; 1BWV.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 90.8%; Score 504; DB 1; Length 108;

Best Local Similarity 91.6%; Pred. No. 8.6e-44;

Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLIGWYQKPKGAPKRLIYAASLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLIGWYQKPKGAPKRLIYAASLSQGVPS 60

QY 61 RFGSGSGTFTTITSSLPQEDPATYCYLQHNSYPLTFGGTKVEIK 107

Db 61 RFSGSGAGTEFTLTIISSLOPEDFATYYCLOONSYPRSGGKVEIK 107

RESULT	2
KVIR_HUMAN	STANDARD; PRT; 108 AA.
ID	P01610;
AC	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation updated)
DE	Ig kappa chain V-I region WEA.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=5606;	[1]
RN	SEQUENCE
RP	MEDLINE=83273707; PubMed=6410398;
RA	Goni F., Frangione B.;
RE	"Amino acid sequence of the Fv region of a human monoclonal IgM
RT	(protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT	in Klebsiella polysaccharides K30 and K33.";
RL	Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC	-I- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC	against 3,4-pyruvylated galactose and isolated from a patient with
CC	Waldenstrom's macroglobulinemia.
DR	PIR; A01876; KIHUWE.
DR	HSSP; P80362; IWL.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPRO07110; Ig-like.
DR	InterPro; IPRO03596; Ig_v.
DR	Pfam; PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Direct protein sequencing; Immunoglobulin V region;
KW	Monoclonal antibody.
FT	DOMAIN 1 23 Framework-1.
FT	DOMAIN 24 34 Complementarity-determining-1.
FT	DOMAIN 35 49 Framework-2.
FT	DOMAIN 50 56 Complementarity-determining-2.
FT	DOMAIN 57 88 Framework-3.
FT	DOMAIN 89 97 Complementarity-determining-3.
FT	DOMAIN 98 107 Framework-4.
FT	DISULFID 23 88 By similarity.
FT	NON_TER 108 108
SQ	SEQUENCE 108 AA; 118940 MW; 9249B61F0945618C CRC64;

OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RI	[1]
RP	SEQUENCE FROM N.A.
RT	TISSUE=Spleen;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Skalswood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Grimwood U., Smalls D.E., Schnertch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RI	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Spleen;
RA	Strausberg R.;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC073791; AAH73791.1; -.
DR	InterPro: IPR003599; Ig.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003597; Ig.C1.
DR	InterPro: IPR003006; Ig.MHC.
DR	InterPro: IPR003596; Ig.V.
DR	Pfam: PF07654; C1-set; 1.
DR	Pfam: PF00047; Ig; 2.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; IgC1; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG LIKE; 2.
DR	PROSITE; PS00290; IG MHC; 1.
KW	Hypothetical protein_1.
QY	SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;
Query Match 89.9%; Score 499; DB 2; Length 236;	
Best Local Similarity 92.5%; Pred. No. 6.8e-43;	
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps	
QY	2 IOWTSPSLASVCDRVTTTCRASQGTINDLWYQKPGKAPKRLIYAASSLQSGVPSR
Db	24 IOWTSPSLASVCDRVTTTCRASQGTINDLWYQKPGKAPKRLIYAASSLQSGVPSR
QY	62 FGSGSGSGTEFTLTISSLQPEDFATYICLQHSNYPLTFGGGTKEIK 107
Db	84 FGSGSGSGTDTFTLTISSLQPEDFATYICLQDNYNPTWTFGGGTKEIK 129
RESULT 4	
Q6GMX8	ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC	Q6GMX8;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]


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RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073764; AAH73764.1; -.
DR InterPro: IPR003599; Ig-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; C1-set; 1.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 85.6%; Score 475; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 1.9e-40;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 82

QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 83 RFSGSGSGTEFTLTISLQPEDFATYYCQQAHSPPFTFGPCTKVDIK 129

RESULT 5
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073764; AAH73764.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; C1-set; 1.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 85.6%; Score 475; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 1.9e-40;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 82

QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 83 RFSGSGSGTEFTLTISLQPEDFATYYCQQAHSPPFTFGPCTKVDIK 129

RESULT 5
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC034141; AAH34141.1; -.
DR HSSP: P01607; 1AR2.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
Query Match 85.0%; Score 472; DB 2; Length 236;
Best Local Similarity 87.9%; Pred. No. 3.9e-40;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDVRVITTCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 82

QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 83 RFSGSGSGTEFTLTISLQPEDFATYYCQQLNSSPPTFGGTKVEIK 129

RESULT 6
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

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RT fetus.";
RL EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSPF; P01607; LBW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 84.5%; Score 469; DB 2; Length 108;
Best Local Similarity 85.0%; Pred. No. 3.3e-40;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIRNDLGYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASQISNYLAWYQKPKVPSKSLIYAASLTLSQSGVPS 60
Qy 61 RFGSGSGTFTLTITSISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107
Db 61 RFGSGSGTFTLTITSISSLPEDVATYYCQKNSAPRTFPGGKLEIK 107

RESULT 7
Q6GMX9 PRELIMINARY; PRT; 236 AA.
ID Q6GMX9
AC Q6GMX9
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
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DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;

Query Match 84.5%; Score 469; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 8e-40;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIRNDLGYQKPKAPKRLIYAASSLSQSGVPS 60
Db 23 DIQWTQSPSSLSASVGRVTTTCRASQNSVSNLAWYQORPEKAPKSLIYATSSLSHSGVPS 82
Qy 61 RFGSGSGTFTLTITSISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107
Db 83 RFGSGSGTFTLTITSISSLPEDFATYYCQVNTYPLTFGGGKVEIK 129

RESULT 8
Q65ZC8 PRELIMINARY; PRT; 244 AA.
ID Q65ZC8
AC Q65ZC8
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RL "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 244 244
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17869338F2BF CRC64;

Query Match 84.3%; Score 468; DB 2; Length 244;
Best Local Similarity 83.2%; Pred. No. 1.1e-39;
Matches 89; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIRNDLGYQKPKAPKRLIYAASSLSQSGVPS 60
Db 137 DIQWTQSPSTLSASTGDRVTTTCRASQIYHNLAWYQKPKAPKFLIYKASSLASGAPS 196
Qy 61 RFGSGSGTFTLTITSISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107
Db 197 RFGSGSGTFTLTITSISSLPEDFATYYCQVSNYPLTFGGGKLEIK 243

RESULT 9
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98375893; PubMed=97112075;
RA Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR ENBL; U96396; AAB68785.1; -
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
SQ
Query Match 83.7%; Score 464.5; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 9.3e-40;
Matches 95; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLWYQKPKAPKRLIYAASSLSQSVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISISLYNWYQKPKAPKRLIYAASSLSQSVPS 60
Qy 61 RFGSGSGTFTLTITSSLPQDPATYCYLOHNSYPLTFGGGTKEIK 107
Db 61 RFGSGSGTFTLTITSSLPQDPATYCYQSYSTLTFFGGGTKEIK 106
RESULT 10
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0
AC Q6GMX0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schnerch A., Schein J.E.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073775; AH73775.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
Query Match 83.1%; Score 461; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 5.3e-39;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLWYQKPKAPKRLIYAASSLSQSVPS 60
Db 23 DIQWTQSPSSLSASVGRVITTCRASQINNNYQLKPKAPNLLIYAASSLSQSVPS 82
Qy 61 RFGSGSGTFTLTITSSLPQDPATYCYLOHNSYPLTFGGGTKEIK 107
Db 83 RFGSGSGTFTLTITSSLPQDPATYCYQSYSTLTFFGGGTKEIK 129
RESULT 11
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
ID Q7Z3Y4
AC Q7Z3Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal Muscle;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schnerch A., Schein J.E.,

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC SEQUENCE FROM N.A.
RA TISSUE=Skeletal Muscle;
RL Strausberg R.;
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 83.1%; Score 461; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 5.3e-39;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB 83 KFSGSGSGTDFLTITISLQPEDFATYYCQYKSPVTFGGTKLEIK 129

RESULT 12
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263;
RT Kontermann R.E., Wing M.G., Winter G.;
RL "Complement recruitment using bispecific diabodies.";
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 82.9%; Score 460; DB 2; Length 240;
Best Local Similarity 82.2%; Pred. No. 6.8e-39;
Matches 88; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
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Db 133 DIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQQKPGKAPKRLIYKASSLSRAP 192
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB 193 RFSGSGSGTDFLTITISLQDDFATYYCQYNSYPLTFGGGTKVEIK 239

RESULT 13
KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTLN.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 82.2%; Score 456; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 7e-39;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB 61 NFGSGSGTDFLTITISLQPEDFATYYCQYNSYPTFGGQTKVQIK 107

RESULT 14
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match      81.8%; Score 454; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 1.1e-38;
Matches 92; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGINDLGWYQQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQISISYLNWYQQKPKAPNLLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTEFTLTISLQPEDFATYICLOHNSVPLTFGGGTVK 107
DB 61 RFSGSGSGTDFLTISLQPEDFATYICQOSYSTSWTFEGGTVK 107

RESULT 15
KVLS HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; KIHWS.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
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FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;

Query Match      81.4%; Score 452; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 1.8e-38;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGINDLGWYQQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDISHLAWYQQKSGKAPKRLIYASLSQGVPS 60
QY 61 RFSGSGSGTEFTLTISLQPEDFATYICLOHNSVPLTFGGGTVK 107
DB 61 RFSGSGSGTEFTLTISLQPEDFATYICQOAHSVPLTFGGGTVK 107

Search completed: November 16, 2005, 22:01:51
Job time : 59.9908 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQHSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	91.4	108	2	US-08-378-939-32
2	507	91.4	108	2	US-08-378-939-34
3	502	90.5	107	3	US-09-240-274-29
4	497	89.5	236	1	US-08-157-101A-5
5	489	88.1	108	3	US-09-025-769B-14
6	489	88.1	108	4	US-09-490-070A-14
7	489	88.1	108	4	US-09-490-153-14
8	489	88.1	108	4	US-09-490-324-14
9	481	86.7	107	2	US-07-934-373C-18
10	481	86.7	107	3	US-08-437-642B-18
11	481	86.7	107	4	US-08-146-206C-18
12	481	86.7	107	4	US-09-648-067A-14
13	481	86.7	107	4	US-09-705-686-18
14	481	86.7	107	4	US-09-705-392A-18
15	481	86.7	107	4	US-09-705-398-18
16	481	86.7	107	5	PCT-US93-07832-18
17	481	86.7	108	2	US-08-379-057-29
18	481	86.7	108	3	US-08-974-899-3
19	481	86.7	108	4	US-09-795-798-3
20	478	86.1	108	3	US-08-974-899-2
21	478	86.1	108	4	US-09-795-798-2
22	478	86.1	109	3	US-09-025-769B-28
23	478	86.1	109	3	US-09-025-769B-43
24	478	86.1	109	4	US-09-490-070A-28
25	478	86.1	109	4	US-09-490-070A-43
26	478	86.1	109	4	US-09-490-153-28
27	478	86.1	109	4	US-09-490-153-43

28	478	86.1	109	4	US-09-490-324-28	Sequence 28, Appl
29	478	86.1	109	4	US-09-490-324-43	Sequence 43, Appl
30	477	85.9	107	3	US-08-599-226-1	Sequence 1, Appl
31	477	85.9	107	3	US-09-125-098-1	Sequence 1, Appl
32	477	85.9	107	4	US-09-540-018-1	Sequence 18, Appl
33	477	85.9	108	2	US-08-378-939-18	Sequence 9, Appl
34	476	85.8	107	3	US-08-599-226-9	Sequence 30, Appl
35	476	85.8	107	3	US-09-125-098-9	Sequence 3, Appl
36	476	85.8	107	4	US-09-540-018-9	Sequence 3, Appl
37	476	85.8	236	4	US-09-859-053-30	Sequence 3, Appl
38	475	85.6	109	2	US-07-934-373C-3	Sequence 3, Appl
39	475	85.6	109	3	US-08-437-642B-3	Sequence 3, Appl
40	475	85.6	109	4	US-08-146-206C-3	Sequence 3, Appl
41	475	85.6	109	4	US-09-705-686-3	Sequence 3, Appl
42	475	85.6	109	4	US-09-705-392A-3	Sequence 3, Appl
43	475	85.6	109	4	US-09-705-398-3	Sequence 3, Appl
44	475	85.6	109	5	PCT-US93-07832-3	Sequence 18, Appl
45	474	85.4	107	3	US-08-871-488A-18	

ALIGNMENTS

RESULT 1
US-08-378-939-32
; Sequence 32, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-32

Query Match 91.4%; Score 507; DB 2; Length 108;
Best Local Similarity 91.6%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLWGYYQOKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLWGYYQOKPGKAPKRLIYAASSLSQGVPS 60


```

RESULT 6
US-09-490-070A-14
; Sequence 14, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
;
US-09-490-070A-14

Query Match      88.1%; Score 489; DB 4; Length 108;
Best Local Similarity 90.7%; Pred.No.7.3e-39;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMOTSPSLASVGDRVTITCRASQGIKNDLIGWYQKQKPGKAPKRLIYAASSLQSGVPS 60
DB 1 DIQMOTSPSLASVGDRVTITCRASQISNLYLNWYQKQKPGKAPKRLIYAASSLQSGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDPATYCYLOHNSYPLTFGGGTQVKEIK 107
DB 61 RFSGSGSGTDFTLTISSLQPEDPATYCYQOYSTPLTFGGGTQVKEIK 107

RESULT 7
US-09-490-153-14
; Sequence 14, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming

```

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries
;; NUMBER OF SEQUENCES: 373
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/490,153
;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-153-14

Query Match 88.1%; Score 489; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 7.3e-39;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTITCRASQSIISNLYNWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGGTFTLTISLSQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFGSGSGGTFTLTISLSQPEDFATYYCQYYSTPLTFGGGTKVEIK 107

RESULT 8
US-09-324-14
; Sequence 14, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/490,324
;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-324-14

Query Match 88.1%; Score 489; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 7.3e-39;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTITCRASQSIISNLYNWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGGTFTLTISLSQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFGSGSGGTFTLTISLSQPEDFATYYCQYYSTPLTFGGGTKVEIK 107

RESULT 9
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-07-934-373C-18
Query Match 86.7%; Score 481; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVITCRASQSIKNLWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107

RESULT 10
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-437-642B-18
Query Match 86.7%; Score 481; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVITCRASQSIKNLWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107

RESULT 11
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-146-206C-18
Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVITCRASQSIKNLWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISSLPQEDFATYCCQYNSLPWTFGGTKVEIK 107
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RESULT 12
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: PI775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR FILING DATE: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQIRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLAWYQKPGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107

RESULT 13
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-NO. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQIRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLAWYQKPGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107

RESULT 14
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-NO. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQIRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNLYAWYQQKFGKAPKLLIYAASSLESQVPS 60
Qy 61 RFGSGSGTFTLTITSSLPEDFATYYCLQHNYSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPEDFATYYCQYNLSLPTWTFGGTKVEIK 107

RESULT 15

US-09-705-398-18
; Sequence 18, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-6800738-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-Nov-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGMWYQQKFGKAPKRLIYAASSLSQVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNLYAWYQQKFGKAPKLLIYAASSLESQVPS 60
Qy 61 RFGSGSGTFTLTITSSLPEDFATYYCLQHNYSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPEDFATYYCQYNLSLPTWTFGGTKVEIK 107

Search completed: November 16, 2005, 22:07:19
Job time : 19.1939 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-14
Perfect score: 555
Sequence: 1 DIQMTSPSLASVGDVRT.....CLQHNSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	555	100.0	107	14	US-10-330-613-14
2	555	100.0	107	14	US-10-330-530-14
3	555	100.0	107	14	US-10-041-860-18
4	555	100.0	107	14	US-10-041-860-233
5	555	100.0	107	14	US-10-041-860-267
6	555	100.0	107	14	US-10-041-860-285
7	555	100.0	107	15	US-10-309-762-51
8	555	100.0	107	16	US-10-660-357-14
9	555	100.0	107	16	US-10-665-383-16
10	555	100.0	107	17	US-10-727-155-208
11	555	100.0	107	17	US-10-727-155-220
Sequence 14, Appl					
Sequence 14, Appl					
Sequence 18, Appl					
Sequence 233, Appl					
Sequence 267, Appl					
Sequence 285, Appl					
Sequence 51, Appl					
Sequence 14, Appl					
Sequence 16, Appl					
Sequence 208, Appl					
Sequence 220, Appl					

12	555	100.0	107	17	US-10-727-155-273	Sequence 273, App
13	555	100.0	107	17	US-10-727-155-305	Sequence 305, App
14	555	100.0	107	17	US-10-877-773-24	Sequence 24, Appl
15	555	100.0	107	17	US-10-877-774-24	Sequence 24, Appl
16	555	100.0	108	17	US-10-805-177-62	Sequence 62, Appl
17	554	99.8	108	17	US-10-805-177-4	Sequence 4, Appl
18	554	99.8	168	17	US-10-805-177-115	Sequence 115, App
19	552	99.5	107	17	US-10-727-155-4	Sequence 4, Appl
20	552	99.5	107	17	US-10-727-155-28	Sequence 28, Appl
21	551	99.3	107	14	US-10-041-860-14	Sequence 14, Appl
22	551	99.3	107	14	US-10-041-860-229	Sequence 229, App
23	551	99.3	107	14	US-10-041-860-263	Sequence 263, App
24	551	99.3	107	16	US-10-665-383-8	Sequence 8, Appl
25	551	99.3	107	17	US-10-727-155-224	Sequence 224, App
26	551	99.3	107	17	US-10-893-576-176	Sequence 176, App
27	551	99.3	129	17	US-10-893-576-40	Sequence 40, Appl
28	548	98.7	107	15	US-10-309-762-57	Sequence 57, Appl
29	548	98.7	107	17	US-10-727-155-8	Sequence 8, Appl
30	548	98.7	153	15	US-10-309-762-245	Sequence 245, App
31	547	98.6	107	17	US-10-727-155-12	Sequence 12, Appl
32	546	98.4	107	17	US-10-727-155-32	Sequence 32, Appl
33	546	98.4	107	17	US-10-727-155-126	Sequence 126, App
34	546	98.4	107	17	US-10-893-576-175	Sequence 175, App
35	546	98.4	129	17	US-10-893-576-34	Sequence 34, Appl
36	544	98.0	107	15	US-10-309-762-58	Sequence 58, Appl
37	544	98.0	107	16	US-10-684-109-57	Sequence 57, Appl
38	544	98.0	234	16	US-10-684-109-115	Sequence 115, App
39	543	97.8	107	17	US-10-727-155-256	Sequence 256, App
40	543	97.8	110	16	US-10-312-316-52	Sequence 52, Appl
41	542	97.7	107	17	US-10-727-155-40	Sequence 40, Appl
42	542	97.7	107	17	US-10-727-155-44	Sequence 44, Appl
43	542	97.7	107	17	US-10-727-155-78	Sequence 78, Appl
44	542	97.7	107	17	US-10-727-155-252	Sequence 252, App
45	541	97.5	107	14	US-10-330-613-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-330-613-14
; Sequence 14, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-14

Query Match	100.0%;	Score	555;	DB	14;	Length	107;
Best Local Similarity	100.0%;	Pred. No.	9e-40;				
Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	DIQMTSPSLASVGDVRTVITCRASQGI	RNDLGTWQKPKGKAPKRLIYAASSLSQGVPS	60			
Db	1	DIQMTSPSLASVGDVRTVITCRASQGI	RNDLGTWQKPKGKAPKRLIYAASSLSQGVPS	60			
Qy	61	RFGSGSGTGTEFTLTISLQPEDPATY	YCLQHNSYPLTFGGTKVEIK	107			
Db	61	RFGSGSGTGTEFTLTISLQPEDPATY	YCLQHNSYPLTFGGTKVEIK	107			

RESULT 2

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US-10-330-530-14
; Sequence 14, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Cudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-330-530-14

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 3
US-10-041-860-18
; Sequence 18, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-18

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 4
US-10-041-860-233
; Sequence 18, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-233

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
```

```
; Sequence 233, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-233

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 5
US-10-041-860-267
; Sequence 267, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-267

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
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Db 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 6

US-10-041-860-285
; Sequence 285, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-285

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 7

US-10-309-762-51
; Sequence 51, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309.762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-51

Query Match 100.0%; Score 555; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 8

US-10-660-357-14
; Sequence 14, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660.357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330.580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-14

Query Match 100.0%; Score 555; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTITSSLPQEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 9

US-10-665-383-16
; Sequence 16, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Larochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: AGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665.383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411.137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-16

Query Match 100.0%; Score 555; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 10

US-10-727-155-208
; Sequence 208, Application US/10727155
; Publication No. US20050049402A1

GENERAL INFORMATION:

; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchro
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS

; TITLE OF INVENTION: FACTOR AND USES THEREOF

; FILE REFERENCE: AGENIX.073A

; CURRENT APPLICATION NUMBER: US/10/727,155

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: 60/430729

; PRIOR FILING DATE: 2002-12-02

; NUMBER OF SEQ ID NOS: 320

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 208

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-727-155-208

Query Match 100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 11

US-10-727-155-220
; Sequence 220, Application US/10727155
; Publication No. US20050049402A1

GENERAL INFORMATION:

; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchro
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi

; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: AGENIX.073A

; CURRENT APPLICATION NUMBER: US/10/727,155

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: 60/430729

; PRIOR FILING DATE: 2002-12-02

; NUMBER OF SEQ ID NOS: 320

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 220

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-727-155-220

Query Match 100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 12

US-10-727-155-273

; Sequence 273, Application US/10727155

; Publication No. US20050049402A1

; GENERAL INFORMATION:

; APPLICANT: John S. Babcock

; APPLICANT: Jaspal S. Kang

; APPLICANT: Orit Foord

; APPLICANT: Larry Green

; APPLICANT: Xiao Feng

; APPLICANT: Scott Klakamp

; APPLICANT: Mary Haak-Frendscho

; APPLICANT: Palaniswami Rathanaswami

; APPLICANT: Craig Pigott

; APPLICANT: Meina Liang

; APPLICANT: Rozanne Lee

; APPLICANT: Kathy Manchulenchro

; APPLICANT: Raffaella Faggioni

; APPLICANT: Giorgio Senaldi

; APPLICANT: Qiaojuan Jane Su

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS

; TITLE OF INVENTION: FACTOR AND USES THEREOF

; FILE REFERENCE: AGENIX.073A

; CURRENT APPLICATION NUMBER: US/10/727,155

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: 60/430729

; PRIOR FILING DATE: 2002-12-02

; NUMBER OF SEQ ID NOS: 320

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 273

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-727-155-273

Query Match 100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

Db 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
RESULT 13
US-10-727-155-305
; Sequence 305, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-305
Query Match 100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60
Qy 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
RESULT 14
US-10-727-773-24
; Sequence 24, Application US/10877773
; Publication No. US20050053608A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Rava, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; FILE REFERENCE: ABGENIX.087A2
; CURRENT APPLICATION NUMBER: US/10877,774
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-773-24

; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; FILE REFERENCE: ABGENIX.087A
; CURRENT APPLICATION NUMBER: US/10877,773
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-773-24
Query Match 100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60
Qy 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIK 107
RESULT 15
US-10-877-774-24
; Sequence 24, Application US/10877774
; Publication No. US20050059087A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Rava, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; FILE REFERENCE: ABGENIX.087A2
; CURRENT APPLICATION NUMBER: US/10877,774
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-774-24

```

Query Match      100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLQSGVPS 60
   |||||||
Db 1 DIQMTQSPSSLSASVGDRTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLQSGVPS 60
   |||||||

Qy 61 RFSGSGGTFTLTISSLQPEDFATYVCLQHNSEYPLTFGGGTKVEIK 107
   |||||||
Db 61 RFSGSGGTFTLTISSLQPEDFATYVCLQHNSEYPLTFGGGTKVEIK 107
   |||||||

```

Search completed: November 16, 2005, 23:05:41
Job time : 66.6949 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPWTFGGTKVIEK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_16Dec04:*
- 2: Geneseqp1980s:*
- 3: Geneseqp1990s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2001s:*
- 6: Geneseqp2002s:*
- 7: Geneseqp2003as:*
- 8: Geneseqp2003bs:*
- 9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	7	ADC99789 Anti-huma
2	561	100.0	107	7	ADD05393
3	561	100.0	107	7	ADFO9831 Human ant
4	561	100.0	107	7	ADK18842 Anti-huma
5	561	100.0	107	7	ADK18916 Anti-huma
6	561	100.0	107	7	ADK18892 Anti-huma
7	561	100.0	107	7	ADK18612 Anti-huma
8	561	100.0	107	7	ADK18602 Anti-huma
9	561	100.0	107	7	ADK18810 Anti-huma
10	561	100.0	107	7	ADK18844 Anti-huma
11	561	100.0	107	7	ADK18808 Anti-huma
12	561	100.0	107	7	ADK18807 Anti-huma
13	561	100.0	107	7	ADK18604 Anti-huma
14	561	100.0	107	7	ADP03996 Murine-ex
15	561	100.0	107	8	ADL25422 Human mAb
16	561	100.0	107	8	ADL25426 Human mAb
17	561	100.0	107	8	ADL25442 Human mAb
18	561	100.0	107	8	ADDO7289 Human pro
19	561	100.0	107	8	ADP22368 Human ant
20	561	100.0	107	8	ADP22401 Human ant
21	561	100.0	236	5	ABG77164 Germline
22	561	100.0	236	8	ADR28586 Human ant
23	558	99.5	107	7	ADK18841 Anti-huma
24	556	99.1	107	8	ADP22158 Human ant
25	551	98.2	107	7	ADK18885 Anti-huma

26	549	97.9	107	8	ADP22110 Human ant
27	549	97.9	107	8	ADP22354 Human ant
28	549	97.9	236	5	ABG77160 Germline
29	549	97.9	236	8	ADR28582 Human ant
30	548	97.7	107	7	ADK18840 Anti-huma
31	548	97.7	107	7	ADK18879 Anti-huma
32	548	97.7	107	7	ADK18806 Anti-huma
33	548	97.7	107	7	ADK18600 Anti-huma
34	548	97.7	107	8	ADL25418 Human mAb
35	548	97.7	236	8	ADP07905 Human imm
36	547	97.5	107	8	ADP22154 Human ant
37	545	97.3	108	8	ADP47296 Human pho
38	545	97.1	107	7	ADP03916 Murine-ex
39	545	97.1	107	7	ADP03912 Murine-ex
40	545	97.1	107	7	ADP03908 Murine-ex
41	545	97.1	107	7	ADP03913 Murine-ex
42	542	96.6	152	8	ADK52390 Human ant
43	541	96.4	107	7	ADC99785 Anti-huma
44	541	96.4	107	7	ADD05389 Anti-MUC1
45	541	96.4	107	7	ADF09827 Human ant

ALIGNMENTS

RESULT 1

ADC99789
ID ADC99789 standard; protein; 107 AA.

AC ADC99789;

DT 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 18.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytotactic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human.

OS Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

XX WPI; 2003-587113/55.

DR N-PSDB; ADC99791.

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.

XX Claim 3; SEQ ID NO 18; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising
a heavy or light chain amino acid or a heavy or light chain variable
domain where the antibody binds to MUC18. The monoclonal antibody of the
invention demonstrates cytostatic activity and may be useful for treating
a disease or condition associated with the expression of MUC18 on the
cell surface such as tumors, specifically melanoma, oesophageal,
pancreatic or colorectal tumours, carcinomas, particularly cervical
carcinomas and cervical intraepithelial neoplasia and cancers including
colorectal, breast or lung cancer, as well as other malignancies. The
current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.

XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 2

ID ADD05393 standard; protein; 107 AA.
XX
AC ADD05393;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 18.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
DR N-PSDB; ADD05395.
XX
Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 18; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.

XX Sequence 107 AA;

SQ Query Match 100.0%; Score 561; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 3

ID ADF09831 standard; protein; 107 AA.
XX
AC ADF09831;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #5.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
DR N-PSDB; ADF09833.
XX
Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 18; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.

SQ Sequence 107 AA;

Query Match 100.0%; Score 561; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

DB 61 RFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

```
RESULT 4
ADK18942
ID ADK18942 standard; protein; 107 AA.
XX AC ADK18942;
XX
XX 06-MAY-2004 (first entry)
DT XX
DE XX
DE XX
XX Anti-human PDGF-D antibody protein related sequence #68.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
PF XX
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
PR XX
PR 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
PA
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 266; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
DB 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
RESULT 5
ADK18916
ID ADK18916 standard; protein; 107 AA.
XX AC ADK18916;
XX
XX 06-MAY-2004 (first entry)
DT XX
DE XX
DE XX Anti-human PDGF-D antibody protein related sequence #142.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
DB 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
RESULT 6
ADK18992
ID ADK18992 standard; protein; 107 AA.
XX AC ADK18992;
XX
XX 06-MAY-2004 (first entry)
DT XX
DE XX
DE XX Anti-human PDGF-D antibody protein related sequence #119.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
PF XX
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
PR XX
PR 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
PA
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 340; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
DB 61 RFGSGSGTFTLTITSLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
```

PA (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 316; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTETFTLTISLQPEDFATYYCLOHNSYPWTFQGQTKVEIK 107
DB 61 RFGSGSGTETFTLTISLQPEDFATYYCLOHNSYPWTFQGQTKVEIK 107
RESULT 7
ADK18612
ID ADK18612 standard; protein; 107 AA.
AC ADK18612;
XX 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody light chain protein sequence.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 36; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTETFTLTISLQPEDFATYYCLOHNSYPWTFQGQTKVEIK 107
DB 61 RFGSGSGTETFTLTISLQPEDFATYYCLOHNSYPWTFQGQTKVEIK 107
RESULT 8
ADK18602
ID ADK18602 standard; protein; 107 AA.
AC ADK18602;
XX 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody light chain protein sequence.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 26; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX

SQ Sequence 107 AA;
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 9
ADK18810
ID ADK18810 standard; protein; 107 AA.
XX
AC ADK18810;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #36.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 234; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.

SQ Sequence 107 AA;
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 11
ADK18808
ID ADK18808 standard; protein; 107 AA.
XX
AC ADK18808;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #34.

Db 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 10
ADK18844
ID ADK18844 standard; protein; 107 AA.
XX
AC ADK18844;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #70.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 268; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.

SQ Sequence 107 AA;
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGRVITTCRASQIRNDLGYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGTGTEFTLTIISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 11
ADK18808
ID ADK18808 standard; protein; 107 AA.
XX
AC ADK18808;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #34.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX Homo sapiens.
 OS WO2003057857-A2.
 PN 17-JUL-2003.
 PD
 XX
 XX 06-JAN-2003; 2003WO-US000398.
 PF
 XX 07-JAN-2002; 2002US-00041860.
 PR
 XX (ABGE-) ABGENIX INC.
 PA
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR
 XX New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX
 XX Disclosure; SEQ ID NO 232; 255pp; English.
 PS
 XX The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX
 XX Sequence 107 AA;
 SQ
 Query Match 100.0%; Score 561; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.9e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
 DB 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
 QY 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKEIK 107
 DB 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKEIK 107
 RESULT 12
 ADK18807
 ID ADK18807 standard; protein; 107 AA.
 AC ADK18807;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Anti-human PDGF-D antibody protein related sequence #33.
 DE
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX WO2003057857-A2.
 PN
 XX 17-JUL-2003.
 PD
 XX
 XX 06-JAN-2003; 2003WO-US000398.
 PF
 XX 07-JAN-2002; 2002US-00041860.
 PR

XX (ABGE-) ABGENIX INC.
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR
 XX New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX
 XX Disclosure; SEQ ID NO 231; 255pp; English.
 PS
 XX The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX
 XX Sequence 107 AA;
 SQ
 Query Match 100.0%; Score 561; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.9e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
 DB 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
 QY 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKEIK 107
 DB 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKEIK 107
 RESULT 13
 ADK18604
 ID ADK18604 standard; protein; 107 AA.
 AC ADK18604;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Anti-human PDGF-D antibody light chain protein sequence.
 DE
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX WO2003057857-A2.
 PN
 XX 17-JUL-2003.
 PD
 XX
 XX 06-JAN-2003; 2003WO-US000398.
 PF
 XX 07-JAN-2002; 2002US-00041860.
 PR
 XX (ABGE-) ABGENIX INC.
 PA
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR
 XX New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX

The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervix carcinoma,

CC monoclonal antibody (mAb) variable region sequence, which is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 561; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.9e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGVYQOKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGVYQOKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLPEDFATYICLQHSYPTWTFQGQTKVEIK 107

Db 61 RFGSGSGTFTLTITSSLPEDFATYICLQHSYPTWTFQGQTKVEIK 107

Search completed: November 16, 2005, 21:51:38
 Job time : 61.3676 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	93.2	125	S40353	Ig kappa chain V-J
2	521	92.9	108	K1HUWE	Ig kappa chain V-I
3	511	91.1	123	S40313	Ig kappa chain V-J
4	510	90.9	108	K1HUGL	Ig kappa chain V-I
5	495	88.2	125	S40333	Ig kappa chain V-J
6	494	88.1	117	S41809	Ig kappa chain V-I
7	489	87.2	107	S36269	Ig kappa chain V-I
8	488	87.0	107	S36262	Ig kappa chain V-I
9	485	86.5	127	S40367	Ig kappa chain V-J
10	485	86.5	129	S40369	Ig kappa chain - h
11	481.5	85.8	124	S40336	Ig kappa chain V-J
12	480	85.6	126	S40335	Ig kappa chain V-J
13	479	85.4	108	S36279	Ig kappa chain V-I
14	473	84.3	123	S40331	Ig kappa chain - h
15	473	84.3	132	S40334	Ig kappa chain - h
16	472	84.1	114	S46377	Ig kappa chain V-J
17	470	83.8	125	S40349	Ig kappa chain V-J
18	469	83.6	131	S40352	Ig kappa chain V-J
19	467	83.2	95	S69898	Ig kappa chain V-I
20	467	83.2	108	B49047	Ig kappa chain V-I
21	467	83.2	141	R49134	Ig kappa chain V-I
22	466	83.1	108	K1HUBN	Ig kappa chain V-I
23	464	82.7	117	S46371	Ig kappa chain V-J
24	463	82.5	107	T169017	anti-HIV1 envelope
25	463	82.5	124	S40318	Ig kappa chain V-I
26	462	82.4	107	S36264	Ig kappa chain V-I
27	462	82.4	108	S44122	Ig kappa chain V-I
28	461	82.2	108	S19674	Ig kappa chain V-I
29	460.5	82.1	107	S36275	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40353

Ig kappa chain V-J-C region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40353

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40353

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 <KLE>

A/Cross-references: EMBL:X72463

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/30-104/Domain: immunoglobulin homology <IMW>

Query Match 93.2% Score 523; DB 2; Length 125;

Best Local Similarity 94.4%; Pred. No. 2.1e-37;

Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQSGVPS 60

Db 15 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQSGVPS 74

Qy 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107

Db 75 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 121

RESULT 2

K1HUWE

Ig kappa chain V-I region (WEA) - human

C/Species: Homo sapiens (man)

C/Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

C/Accession: A01876

R/Goni, F.; Frangione, B.

Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983

A/Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) wit

A/Reference number: A93964; MUID:83273707; PMID:6410398

A/Accession: A01876

A/Molecule type: protein

A/Residues: 1-108 <GON>

A/Cross-references: UNIPROT:P01610

C/Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 92.9%; Score 521; DB 1; Length 108;
Best Local Similarity 91.6%; Pred. No. 2.7e-37;
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYGATLSQSGVPS 60

Qy 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Db 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 3

S40313

Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40313

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-123 <KLE>

A;Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 511; DB 2; Length 123;
Best Local Similarity 92.5%; Pred. No. 2.1e-36;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 17 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYDAASLLSGVPS 76

Qy 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Db 77 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 123

RESULT 4

KIHUGL

Ig kappa chain V-I region (Gal) - human (tentative sequence)
C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867

R;Laure, C.J.; Watanabe, S.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973

A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I

A;Reference number: A01867; MUID:75059122; PMID:4215718

A;Accession: A01867

A;Molecule type: protein

A;Residues: 1-108 <LAU>

A;Cross-references: UNIPROT:P01599

A;Note: the C region of this chain has the Inv (3) marker

C;Comment: This chain was isolated from a Waldenström's macroglobulin.

C;Genetics:

A;Gene: GDB:IGKV1

A;Cross-references: GDB:136264

A;Map position: 2p12-2p12

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 90.9%; Score 510; DB 1; Length 108;
Best Local Similarity 92.5%; Pred. No. 2.3e-36;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYAASNLQSGVPS 60

Qy 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Db 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 5

S40333

Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40333

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-125 <KLE>

A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 495; DB 2; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.8e-35;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 19 DIQWTPSTLSASVGDRTVITCRASQISSWLAWYQKPKAPKRLIYKASSLESQVPS 78

Qy 61 RFGSGSGTTEFTLTISLQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Db 79 RFGSGSGTTEFTLTISLQPEDFATYYCQYNSYPWTFGGQTKVEIK 125

RESULT 6

S41809

Ig kappa chain V region A30 - human
C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S41809

R;Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zae

Eur. J. Immunol. 23, 2868-2875, 1993

A;Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequence

A;Reference number: S41809; MUID:94039386; PMID:8223863

A;Accession: S41809

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <HUB>

A;Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384

C;Genetics:

A;Introns: 19/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 494; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.5e-35;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 82
Qy 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYP 95
Db 83 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYP 117

RESULT 7

S40369
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36269
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36269
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <GRI>
A/Cross-references: EMBL:Z18838; NID:933422; PIDN:CAA79290.1; PID:g939915
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 489; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.3e-34;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYTSSLSQGVPS 60
Qy 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKLEIK 107

RESULT 8

S36262
Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36262
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36262
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <GRI>

A/Cross-references: EMBL:Z18842
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 488; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 1.6e-34;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIVMTQSPSSLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSLPPTFGGTKVEIK 107

RESULT 9

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-127 <KLE>

A/Cross-references: EMBL:X72477

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 485; DB 2; Length 127;
Best Local Similarity 88.8%; Pred. No. 3.4e-34;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 18 DIQWTSPLSASVGRVITTCRASQISNLYNWYQKPKAPKRLIYAASSLSQGVPS 77

Qy 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

Db 78 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 124

RESULT 10

S40369
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40369
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40369

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-129 <KLE>

A/Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:g441427

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 485; DB 2; Length 129;
Best Local Similarity 87.9%; Pred. No. 3.4e-34;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 22 DIQWTSPLSASVGRVITTCRASVISHLVFWQKPKAPKRLIYAASSLSQGVPS 81

Qy 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

Db 82 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPVTFGGTKLEIK 128

RESULT 11

S40336
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40336
R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMW>

Query Match 85.8%; Score 481.5; DB 2; Length 124;
Best Local Similarity 88.0%; Pred. No. 6.5e-34;
Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 16 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 75

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 107
Db 76 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 123

RESULT 12
S40335
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40335
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40335
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: EMBL:X72445
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMW>

Query Match 85.6%; Score 480; DB 2; Length 126;
Best Local Similarity 85.8%; Pred. No. 8.9e-34;
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPSR 61
Db 17 IQMTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPSR 76

Qy 62 FSGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 107
Db 77 FSGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKLEMK 122

RESULT 13
S36279
Ig lambda chain V region (clone alpha-THY-23) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36279
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36279
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <GRI>
A:Cross-references: EMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID:g939911
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match 85.4%; Score 479; DB 2; Length 108;
Best Local Similarity 86.9%; Pred. No. 9.3e-34;
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 107
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKLEIK 107

RESULT 14
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMW>

Query Match 84.3%; Score 473; DB 2; Length 123;
Best Local Similarity 88.8%; Pred. No. 3.4e-33;
Matches 95; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 17 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 76

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 107
Db 77 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGGQTKVEIK 123

RESULT 15
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMW>

Query Match 84.3%; Score 473; DB 2; Length 132;
Best Local Similarity 85.0%; Pred. No. 3.6e-33;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 22 DIQLTQSPFLSASIGDRVTITCRASQGINSYLAWYQQKPKAPKLLIYVASTLQSGVPS 81

Oy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107

Db 82 RFSGSGGTEFTLTISLQPEDFASYYCQGFNSYPFTFGGGTKVEIR 128

Search completed: November 16, 2005, 22:04:08
Job time : 13.7849 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQNSYPWTFQGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	521	92.9	108	1 KV1R_HUMAN	P01610 homo sapien
2	519	92.5	236	2 Q6GMW1	Q6gmw1 homo sapien
3	510	90.9	108	1 KV1G_HUMAN	P01599 homo sapien
4	477	85.0	236	2 Q6GMX8	Q6gmx8 homo sapien
5	471	84.0	108	2 Q9UL77	Q9ul77 homo sapien
6	469	83.6	108	2 Q9UL70	Q9ul70 homo sapien
7	466	83.1	108	1 KV1V_HUMAN	P04430 homo sapien
8	464	82.7	236	2 Q7Z3Y4	Q7z3y4 homo sapien
9	463	82.5	236	2 Q6PIH7	Q6pih7 homo sapien
10	455	81.1	236	2 Q6GMX9	Q6gmx9 homo sapien
11	454	80.9	244	2 Q65ZC8	Q65zc8 homo sapien
12	452	80.6	108	1 KV1H_HUMAN	P01600 homo sapien
13	450.5	80.3	107	2 Q6S5S9	Q6s5s9 homo sapien
14	450	80.2	108	1 KV1B_HUMAN	P01594 homo sapien
15	447	79.7	108	1 KV1F_HUMAN	P01598 homo sapien
16	447	79.7	234	2 Q7Z473	Q7z473 homo sapien
17	447	79.7	236	2 Q6GMX0	Q6gmx0 homo sapien
18	446	79.5	129	1 KV1W_HUMAN	P04431 homo sapien
19	446	79.5	240	2 Q65ZC9	Q65zc9 homo sapien
20	444	79.1	236	2 Q6PIT5	Q6pit5 homo sapien
21	440	78.4	108	2 Q9UL79	Q9ul79 homo sapien
22	439	78.3	108	1 KV1L_HUMAN	P01604 homo sapien
23	438	78.1	108	1 KV1S_HUMAN	P01611 homo sapien
24	436	77.7	108	1 KV1M_HUMAN	P01605 homo sapien
25	435	77.5	108	1 KV1O_HUMAN	P01607 homo sapien
26	434.5	77.5	107	1 KV1D_HUMAN	P01596 homo sapien
27	433.5	77.3	107	2 Q9UL81	Q9ul81 homo sapien
28	433	77.2	108	1 KV1C_HUMAN	P01595 homo sapien
29	433	77.2	117	1 KV1I_HUMAN	P01601 homo sapien
30	432	77.0	108	1 KV1E_HUMAN	P01597 homo sapien
31	431	76.8	108	1 KV1Y_HUMAN	P80362 homo sapien

32	431	76.8	129	1 KV1X_HUMAN	P04432 homo sapien
33	430	76.6	108	1 KV1Q_HUMAN	P01609 homo sapien
34	430	76.6	236	2 Q6PIH4	Q6pih4 homo sapien
35	426	75.9	108	1 KV1K_HUMAN	P01603 homo sapien
36	425	75.8	108	1 KV1N_HUMAN	P01606 homo sapien
37	423	75.4	108	1 KV1P_HUMAN	P01608 homo sapien
38	420	74.9	117	1 KV1J_HUMAN	P01602 homo sapien
39	419	74.7	108	1 KV1A_HUMAN	P01593 homo sapien
40	411	73.3	116	2 Q96PF6	Q96pf6 homo sapien
41	404	72.0	108	1 KV5S_MOUSE	P01652 mus musculus
42	401	71.5	108	1 KV5Q_MOUSE	P01653 mus musculus
43	401	71.5	108	1 KV5T_MOUSE	P04207 homo sapien
44	399.5	71.2	129	1 KV3H_HUMAN	P01612 homo sapien
45	396.5	70.7	109	1 KV1T_HUMAN	

ALIGNMENTS

RESULT 1

ID KV1R_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.
RT "Amino acid sequence of the Fv region of a human monoclonal Igm
in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
against 3,4-pyruvylated galactose and isolated from a patient with
Waldenstrom's macroglobulinemia.
DR PIR; A01876; KIHUWE.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody. 23
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 9249B61F0945618C CRC64;

Query Match 92.9%; Score 521; DB 1; Length 108;

Best Local Similarity 91.6%; Pred. No. 9.8e-46;

Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASGIRNDLGTWYQKPKGKAPKRLIYAASSIQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASGIRNDLGTWYQKPKGKAPKRLIYGATLSQSGVPS 60

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Oy 61 RFGSGSGTEFTLTISSLQPEDFATYYCLQHSNYPWTFGGQTKVEIK 107
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTEFTLTINSLPEDFATYYCLQYSSPWFPGQTKVEVK 107

RESULT 2
ID Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RS SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 92.5%; Score 519; DB 2; Length 236;
Best Local Similarity 94.3%; Pred. No. 3.7e-45;
Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKGKPKRLIYAASSLSQGVPSR 61
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 IQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKGKPKRLIYAASSLSQGVPSR 83

Oy 62 FSGSGSGTEFTLTISSLQPEDFATYYCLQHSNYPWTFGGQTKVEIK 107
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 FSGSGSGTEFTLTISSLQPEDFATYYCLQDYNYPWTFGGQTKVEIK 129
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RESULT 3
KVIG HUMAN STANDARD; PRT; 108 AA.
ID KVIG_HUMAN
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."
RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
DR PIR; A01867; K1HUGL.
DR HSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 90.9%; Score 510; DB 1; Length 108;
Best Local Similarity 92.5%; Pred. No. 1.3e-44;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKGKPKRLIYAASSLSQGVPS 60
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLTWYQKPKGKPKRLIYAASNLSQGVPS 60

Oy 61 RFGSGSGTEFTLTISSLQPEDFATYYCLQHSNYPWTFGGQTKVEIK 107
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTEFTLTISSLQPEDFATYYCLQNSYPSRFGQTKVEIK 107

RESULT 4
O6GMX8 PRELIMINARY; PRT; 236 AA.
ID O6GMX8
AC O6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mandina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2].
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073764; AAH73764.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 85.0%; Score 477; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 7.8e-41;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 23 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 82

Qy 61 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVEIK 107
Db 83 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVDIK 129

RESULT 5
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035044; AAD56280.1; -.
DR PIR; P01607; IBMW.
DR HSSP; P01607; B49047.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.0%; Score 471; DB 2; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.3e-40;
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVEIK 107

RESULT 6
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035044; AAD56280.1; -.
DR PIR; P01607; IBMW.
DR HSSP; P01607; B49047.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 83.6%; Score 469; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 2.2e-40;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLOPEDFATYTCLOHNSYPWTFGGTKVEIK 107

```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-Bet; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 82.7%; Score 464; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 1.7e-39;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLGVYQKPGKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTQSPSSLSASVGRVTITCRASQDINSYLAWFQKPGKAPKSLIYDASTLSQGVPS 82

Qy 61 RFGSGSGTETLTITSSLOPEDFATYCYLOHNSYPTWTFGGTKVEIK 107
Db 83 KFGSGSGTDFLTITSSLOPEDFATYCYQKYKSPYPTFGQTKLEIK 129

RESULT 9
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA KVID_HUMAN STANDARD; PRT; 108 AA.
AC P0430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Duillet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSP; P80362; IWLTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR AMYLOID; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3PD944FE96FD37 CRC64;

Query Match 83.1%; Score 466; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 4.4e-40;
Matches 88; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLGVYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQLTQSPSSLSASVGRVTITCRASQSVYVAVFQKPGKAPKSLIYDASTLSQGVPS 60

Qy 61 RFGSGSGTETLTITSSLOPEDFATYCYLOHNSYPTWTFGGTKVEIK 107
Db 61 NFGTSGSGTDFLTITSSLOPEDFATYCYQKYNSPYPTFGQTKVQIK 107

RESULT 8
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -;
DR HSP; P01607; IAR2
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
Query Match 82.5%; Score 463; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 2.1e-39;
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQWTPSPSLASVGRVVTITCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 60
DB 23 DIQWTPSPSLASVGRVVTITCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 82
QY 61 RFSGSGSGTFTLTISLQPEDFATYCYLQHNYPWTFGGGTVK 107
DB 83 RFSGSGSGTFTLTISLQPEDFATYCYLQHNYPWTFGGGTVK 129
RESULT 10
ID Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Ruben G.M., Hong L.,
RA Skaplechno M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;
Query Match 81.1%; Score 455; DB 2; Length 236;
Best Local Similarity 83.2%; Pred. No. 1.4e-38;
Matches 89; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
QY 1 DIQWTPSPSLASVGRVVTITCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 60
DB 23 DIQWTPSPSLASVGRVVTITCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 82
QY 61 RFSGSGSGTFTLTISLQPEDFATYCYLQHNYPWTFGGGTVK 107
DB 83 RFSGSGSGTFTLTISLQPEDFATYCYLQHNYPWTFGGGTVK 129
RESULT 11
ID Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
RA EMBL; Y13057; CAA73500.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG LIKE; 2.
FT NON_TER 1 244
FT SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
SQ

Query Match 80.9%; Score 454; DB 2; Length 244;
Best Local Similarity 81.3%; Pred. No. 1.9e-38;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 137 DIQMTQSPSTLSASIGDRVTITCRASEGIYHMLAWYQKPGKAPKFLIYKASSLASGAPS 196

Qy 61 RFSGSGSTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107
Db 197 RFSGSGSGTDTLTITSSLPQDFATYYCQYQSNVPLTFGGGTKEIK 243

RESULT 12
KV1B_HUMAN
AC KV1B_HUMAN STANDARD; PRT; 108 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=71032830; PubMed=4097974;
RX Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1HUHU.
DR PDB; 1P6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFD 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.6%; Score 452; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 1.2e-38;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISISSYLSWYQKPGKAPQVLIYAASSLPSGVP 60

Qy 61 RFSGSGSTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107
Db 61 RFSGSGSGTDTLTITSSLPQDFATYYCQYQSNVPLTFGGGTKEIK 107

RESULT 13

Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes";
RL J. Immunol. 161:2020-2031 (1998).
DR EMBL; U96396; AB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSPF; P01607; 18WW.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 80.3%; Score 450.5; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.7e-38;
Matches 93; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISISSYLSWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107
Db 61 RFSGSGSGTDTLTITSSLPQDFATYYCQYQSNVPLTFGGGTKEIK 106

RESULT 14
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au)";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,

RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -I- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PR; A91653; KIHUAV.
DR PDB; 1JVS; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.

FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 5
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 80.2%; Score 450; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.9e-38;
Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTFTLTISLQPEDPATYCYLQHSYPTWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTISLQPEDPATYCYLQHSYPTWTFGGQTKVEIK 107

RESULT 15

KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN RN
RX MEDLINE=71064023; PubMed=5489770;
RA Gattlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RN RN
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PR; A90562; KIHUEU.
DR HSP; P01607; IBMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 79.7%; Score 447; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 3.9e-38;
Matches 88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTFTLTISLQPEDPATYCYLQHSYPTWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTISLQPEDPATYCYLQHSYPTWTFGGQTKVEIK 107

Search completed: November 16, 2005, 22:01:52
Job time : 60.9908 secs

THE FINE DREAM (1979)

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQWTQSPSSLSASVGDVRT.....CLQHSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	91.0	107	3	US-09-240-274-29
2	501	89.3	107	2	US-07-934-373C-18
3	501	89.3	107	3	US-08-437-642B-18
4	501	89.3	107	4	US-08-146-206C-18
5	501	89.3	107	4	US-09-648-067A-14
6	501	89.3	107	4	US-09-705-686-18
7	501	89.3	107	4	US-09-705-392A-18
8	501	89.3	107	4	US-09-705-398-18
9	501	89.3	107	5	PCT-US93-07832-18
10	501	89.3	108	3	US-08-974-899-3
11	501	89.3	108	4	US-09-785-798-3
12	500	89.1	108	2	US-08-378-939-32
13	500	89.1	108	2	US-08-378-939-34
14	496	88.4	236	4	US-09-859-053-30
15	487	86.8	107	3	US-08-599-226-1
16	487	86.8	107	3	US-09-125-098-1
17	487	86.8	107	4	US-09-540-018-1
18	486	86.6	107	3	US-08-599-226-9
19	486	86.6	107	3	US-09-125-098-9
20	486	86.6	107	4	US-09-540-018-9
21	485	86.5	109	2	US-07-934-373C-3
22	485	86.5	109	3	US-08-437-642B-3
23	485	86.5	109	4	US-08-146-206C-3
24	485	86.5	109	4	US-09-705-686-3
25	485	86.5	109	4	US-09-705-392A-3
26	485	86.5	109	4	US-09-705-398-3
27	485	86.5	109	5	PCT-US93-07832-3

28	484	86.3	107	3	US-08-871-488A-18
29	484	86.3	109	3	US-09-025-769B-28
30	484	86.3	109	3	US-09-025-769B-43
31	484	86.3	109	4	US-09-490-070A-28
32	484	86.3	109	4	US-09-490-070A-43
33	484	86.3	109	4	US-09-490-153-28
34	484	86.3	109	4	US-09-490-153-43
35	484	86.3	109	4	US-09-490-324-28
36	484	86.3	109	4	US-09-490-324-43
37	483	86.1	236	1	US-08-157-101A-5
38	481	85.7	107	2	US-07-934-373C-17
39	481	85.7	107	3	US-08-437-642B-17
40	481	85.7	107	4	US-08-146-206C-17
41	481	85.7	107	4	US-09-705-686-17
42	481	85.7	107	4	US-09-705-392A-17
43	481	85.7	107	4	US-09-705-398-17
44	481	85.7	107	5	PCT-US93-07832-17
45	481	85.7	108	2	US-08-378-939-24

ALIGNMENTS

RESULT 1
US-09-240-274-29
; Sequence 29, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-29

Query Match 93.0%; Score 522; DB 3; Length 107;
Best Local Similarity 93.3%; Pred. No. 9.6e-41;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 3 QMTQSPSSLSASVGDVRTITCRASQGRNDLGMVQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDVRTITCRASQGRNDLGMVQKPGKAPKRLIYATSSLSQSGVPSRF 61
Qy 63 SGSGSGTEFTLTISLQPEDFATYICLQHSYPWTFGGTKVEIK 107
Db 62 SGSGSGTEFTLTISLQPEDSATYICLQHSFPWTFGGTKVEIK 106

RESULT 2
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-18

Query Match 89.3%; Score 501; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGHYQOKKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQOKKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCQYNSLPWTFGQGTKVEIK 107

RESULT 3
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-18

Query Match 89.3%; Score 501; DB 3; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGHYQOKKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQOKKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCQYNSLPWTFGQGTKVEIK 107

RESULT 4
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-08-146-206C-18
Query Match          89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISLQPEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 5
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14
Query Match          89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISLQPEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 6
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-Nov-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
Query Match          89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISLQPEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6713971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
```

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; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-Nov-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
Query Match          89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISLQPEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6713971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
```

```
;
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18
Query Match 89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIINYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 8
US-09-705-398-18
; Sequence 18, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18
Query Match 89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIINYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 9
PCT-US93-07832-18
; Sequence 18, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-18
Query Match 89.3%; Score 501; DB 5; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIINYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 10
US-08-974-899-3
Query Match 89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIINYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQEDFATYYCQYNSLPWTFGGQTKVEIK 107
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; Sequence 3, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-3

Query Match      89.3%; Score 501; DB 3; Length 108;
Best Local Similarity 90.7%; Pred. No. 8.1e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLWYQKFKGKAPKRLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISNYLAWYQKFKGKAPKRLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTGFTLTITISLQPEDFATYVCLQHSYPTWTFGGTKVKEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTGFTLTITISLQPEDFATYVCCQVNSLPWTFGGTKVKEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match      89.3%; Score 501; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 8.1e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLWYQKFKGKAPKRLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISNYLAWYQKFKGKAPKRLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTGFTLTITISLQPEDFATYVCLQHSYPTWTFGGTKVKEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTGFTLTITISLQPEDFATYVCCQVNSLPWTFGGTKVKEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-08-378-939-32
; Sequence 32, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
```

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; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-32

Query Match      89.1%; Score 500; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1e-38;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISNNLAWYQKPGKAPKRLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTFTLTISLQPEDFATYYCQDQNSYPFTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-08-378-939-34
; Sequence 34, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-34

Query Match      89.1%; Score 500; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1e-38;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISNNLAWYQKPGKAPKRLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTFTLTISLQPEDFATYYCQDQNSYPFTFGGTKVEIK 107
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RESULT 14
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match      88.4%; Score 496; DB 4; Length 236;
Best Local Similarity 89.7%; Pred. No. 5.3e-38;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 DIQMTQSPSSVSASVGDRTVITTCRASQGISRLAWYQKPGKAPKRLIYVASSLSQGVPS 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 RFGSGSGTFTLTISLQPEDFATYYCQQANSFPWTFGGTKVEIK 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-08-599-226-1
; Sequence 1, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-599-226-1

Query Match      86.8%; Score 487; DB 3; Length 107;
Best Local Similarity 88.8%; Pred.No.1.5e-37;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIQWTQSPSSLASVGRVITTCRASQGIKNDLGWYQKPKAPKRLIYAASLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSLQPEDPATYICLOHNSYPWTFGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSLQPEDPATYICQRYNRAPYTFGQTKVEIK 107

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Search completed: November 16, 2005, 22:07:19
Job time : 18.1939 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQWTSPLSASVGRVT.....CLOHNSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	14	US-10-330-613-18
2	561	100.0	107	14	US-10-330-530-18
3	561	100.0	107	14	US-10-041-860-26
4	561	100.0	107	14	US-10-041-860-28
5	561	100.0	107	14	US-10-041-860-36
6	561	100.0	107	14	US-10-041-860-231
7	561	100.0	107	14	US-10-041-860-232
8	561	100.0	107	14	US-10-041-860-234
9	561	100.0	107	14	US-10-041-860-266
10	561	100.0	107	14	US-10-041-860-268
11	561	100.0	107	14	US-10-041-860-316

12	561	100.0	107	14	US-10-041-860-340	Sequence 340, App
13	561	100.0	107	15	US-10-309-762-166	Sequence 166, App
14	561	100.0	107	16	US-10-660-357-18	Sequence 18, App
15	561	100.0	107	16	US-10-665-383-32	Sequence 32, App
16	561	100.0	107	16	US-10-665-383-36	Sequence 36, App
17	561	100.0	107	16	US-10-665-383-52	Sequence 52, App
18	561	100.0	107	17	US-10-727-155-274	Sequence 274, App
19	561	100.0	107	17	US-10-727-155-307	Sequence 307, App
20	561	100.0	236	15	US-10-038-591-52	Sequence 52, App
21	561	100.0	236	16	US-10-775-444A-52	Sequence 52, App
22	561	100.0	236	17	US-10-917-073A-6	Sequence 6, App
23	558	99.5	107	14	US-10-041-860-265	Sequence 265, App
24	556	99.1	107	17	US-10-727-155-64	Sequence 64, App
25	551	98.2	107	14	US-10-041-860-309	Sequence 309, App
26	549	97.9	107	17	US-10-727-155-16	Sequence 16, App
27	549	97.9	107	17	US-10-727-155-260	Sequence 260, App
28	549	97.9	236	15	US-10-038-591-48	Sequence 48, App
29	549	97.9	236	16	US-10-775-444A-48	Sequence 48, App
30	548	97.7	107	14	US-10-041-860-24	Sequence 24, App
31	548	97.7	107	14	US-10-041-860-230	Sequence 230, App
32	548	97.7	107	14	US-10-041-860-264	Sequence 264, App
33	548	97.7	107	14	US-10-041-860-303	Sequence 303, App
34	548	97.7	107	16	US-10-665-383-28	Sequence 28, App
35	547	97.5	107	17	US-10-727-155-60	Sequence 60, App
36	546	97.3	107	18	US-10-822-306A-16	Sequence 16, App
37	546	97.3	108	17	US-10-726-332-211	Sequence 211, App
38	545	97.1	107	15	US-10-309-762-53	Sequence 53, App
39	545	97.1	107	15	US-10-309-762-56	Sequence 56, App
40	542	96.6	152	17	US-10-644-277-96	Sequence 96, App
41	541	96.4	107	14	US-10-330-613-14	Sequence 14, App
42	541	96.4	107	14	US-10-330-530-14	Sequence 14, App
43	541	96.4	107	14	US-10-041-860-18	Sequence 18, App
44	541	96.4	107	14	US-10-041-860-233	Sequence 233, App
45	541	96.4	107	14	US-10-041-860-267	Sequence 267, App

ALIGNMENTS

RESULT 1
US-10-330-613-18
; Sequence 18, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-18

Query Match	100.0%;	Score 561;	DB 14;	Length 107;
Best Local Similarity	100.0%;	Pred. No. 1.7e-39;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DIQWTSPLSASVGRVTITCRASQIGIRNDLGMWQKPKAPKRLIYAASSLSQSGVPS	60	
Db	1	DIQWTSPLSASVGRVTITCRASQIGIRNDLGMWQKPKAPKRLIYAASSLSQSGVPS	60	
Qy	61	RFGSGSGTEFTLTITSLQPEDFATYVCLQHNSYPWTFGGTKVEIK	107	
Db	61	RFGSGSGTEFTLTITSLQPEDFATYVCLQHNSYPWTFGGTKVEIK	107	

RESULT 2

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US-10-330-530-18
; Sequence 18, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-18

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 3
US-10-041-860-26
; Sequence 26, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-26

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 4
US-10-041-860-28
; Sequence 28, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-28

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 5
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
```

```
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 5
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTTTCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
```

```
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
RESULT 6
US-10-041-860-231
; Sequence 231, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-231

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 7
US-10-041-860-232
; Sequence 232, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-232

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 8
US-10-041-860-233
; Sequence 233, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-233

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 9
US-10-041-860-266
; Sequence 266, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-266

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
```

```
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 8
US-10-041-860-234
; Sequence 234, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-234

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 9
US-10-041-860-266
; Sequence 266, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-266
```

```
Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107

RESULT 10
US-10-041-860-268
; Sequence 268, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-268

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107

RESULT 11
US-10-041-860-316
; Sequence 316, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
```

```
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-316

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107

RESULT 12
US-10-041-860-340
; Sequence 340, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-340

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTSPLSASVGDVRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPWTFGQGTKVEIK 107

RESULT 13
US-10-309-762-166
; Sequence 166, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
```

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; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-166

Query Match      100.0%; Score 561; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 14
US-10-660-357-18
; Sequence 18, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-18

Query Match      100.0%; Score 561; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 15
US-10-665-383-32
; Sequence 32, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: AGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
```

```
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-32

Query Match      100.0%; Score 561; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTTEFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Search completed: November 16, 2005, 23:05:42
Job time : 66.6949 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.8088 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-22
Perfect score: 590
Sequence: 1 DIVWTQSPDSLAVSIGERAT.....COQYVSTRPFCQGTWVEIK 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	7	Adc99793 Anti-huma
2	590	100.0	113	7	Adf05397 Anti-MUC1
3	590	100.0	113	7	Adf09835 Human ant
4	556	94.2	133	1	Aap80894 V region
5	550	93.2	114	8	Ado36363 Intracell
6	549	93.1	122	8	Adi26708 Human ant
7	546	92.5	114	8	Adp03687 Human ant
8	546	92.5	114	8	Adp03713 Human ant
9	546	92.5	120	4	Aag65565 Amino aci
10	546	92.5	135	3	Aab03714 Immunoglo
11	546	92.5	135	6	Ada47343 Human ant
12	546	92.5	135	7	Adb72875 Human AAA
13	546	92.5	135	8	Adp88458 Human ant
14	546	92.5	135	8	Adq87927 Human HSI
15	546	92.5	286	8	Adp03811 Human ant
16	544	92.2	114	8	Ado32154 Mouse ant
17	544	92.2	114	8	Adq75236 Immunoglo
18	544	92.2	155	2	Aaw32483 Kappa lig
19	544	92.2	155	2	Aay06912 Human var
20	544	92.2	342	2	Aaw32482 Growth fa
21	544	92.2	342	2	Aay06909 TLHL amin
22	544	92.2	495	2	Aaw32480 Growth fa
23	544	92.2	495	2	Aay06908 CATAB-TEV
24	543	92.0	114	8	Adp03705 Human ant
25	543	92.0	114	8	Adp03709 Human ant

26	543	92.0	114	8	ADP03683	Adp03683 Human ant
27	543	92.0	114	8	ADP03695	Adp03695 Human ant
28	543	92.0	179	8	ADK52434	Adk52434 Human ant
29	542	91.9	252	8	ADO58062	Ado58062 S2 cell d
30	541	91.7	240	4	AAU0815	Aau0815 Human Imm
31	540	91.5	113	8	ADP03723	Adp03723 Human ant
32	540	91.5	119	5	ABE07172	Abb07172 ebvHlgM M
33	540	91.5	119	8	ADI26660	Adi26660 Human ant
34	540	91.5	264	5	ABP43142	Abp43142 Human ova
35	540	91.5	283	8	ADP03815	Adp03815 Human ant
36	539.5	91.4	115	7	ADL91336	Adl91336 VL chain
37	539	91.4	114	2	AAR30144	Aar30144 MAB GAH v
38	539	91.4	114	6	ABP98692	Abp98692 Human GAH
39	539	91.4	114	6	ABP98684	Abp98684 Human GAH
40	539	91.4	114	7	ADG43870	Adg43870 Human pro
41	539	91.4	114	8	ADP03701	Adp03701 Human ant
42	539	91.4	114	8	ADQ28267	Adq28267 Method of
43	538	91.2	113	6	ABJ18724	Abj18724 Antibody
44	538	91.2	114	6	ABJ18682	Abj18682 Antibody
45	538	91.2	115	2	AAW27546	Aaw27546 Human AB

ALIGNMENTS

RESULT 1
ADC99793
ID ADC99793 standard; protein; 113 AA.
XX
AC ADC99793;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 22.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
FN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
XX
DR N-PSDB; ADC99795.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 3; SEQ ID NO 22; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 2
ID ADD05397 standard; protein; 113 AA.
XX
AC ADD05397;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 22.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR N-PSDB; ADD05399.
XX
PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 22; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 3
ID ADF09835 standard; protein; 113 AA.
XX
AC ADF09835;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #6.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
DR N-PSDB; ADF09837.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 22; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
```

```
RESULT 4
AAP80894
ID AAP80894 standard; protein; 133 AA.
XX
XX AAP80894;
AC AAP80894;
XX
XX 25-MAR-2003 (revised)
DT 03-DEC-1990 (first entry)
DE
DE V region of L chain of anti-P.aeruginosa exotoxin Ab #1.
XX
XX Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal peptide
FT Region 21..133
FT /label= V region of L chain
XX
XX EP270077-A.
XX
XX 08-JUN-1988.
XX
XX 01-DEC-1987; 87EP-00117760.
XX
XX 03-DEC-1986; 86JP-00288340.
XX
XX 26-NOV-1987; 87JP-00298513.
XX
XX (SUMO ) SUMITOMO CHEM IND KK.
XX
XX (SUMO ) SUMITOMO PHARM CO LTD.
XX
XX Nakatani T, Nomura N, Horigome K, Noguchi H;
XX
XX WPI; 1988-156310/23.
XX
XX N-PSDB; AAN80499.
XX
XX New gene coding for antibody to Pseudomonas aeruginosa exotoxin - plus
XX recombinant vectors and host cells, useful for treating infections.
XX
XX Claim 4; Page 25; 39pp; English.
XX
XX Sequence is variable region of light chain of anti-exotoxin antibody with
XX signal sequence. AAN80498 encodes the same sequence except that its
XX signal peptide-encoding sequence contains an intron. See also AAN80495-
XX N80496, AAN80498 and AAN80941-2. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX SQ Sequence 133 AA;
Query Match 94.2%; Score 556; DB 1; Length 133;
Best Local Similarity 93.8%; Pred. No. 2.3e-39;
Matches 106; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYVYCOQYVSTPRSGGQVTWEIK 113
Db 81 ESGVPAFSGSGGTDFTLTINSQAEDVAVYVYCOQYVSTPRSGGQVTWEIK 133
RESULT 5
ADO36363
ID ADO36363 standard; protein; 114 AA.
XX
XX ADO36363;
AC ADO36363;
XX
XX 26-AUG-2004 (first entry)
DT
```

```
XX Intracellular interaction-related scFv protein SeqID27.
DE immunoglobulin single domain; intracellular environment;
XX intracellular interaction; immunoglobulin domain; scFv;
KW single chain variable fragment.
XX
XX Unidentified.
OS
XX WO2004046185-A2.
PN
XX 03-JUN-2004.
PD
XX 14-NOV-2003; 2003WO-GB004942.
PF
XX 15-NOV-2002; 2002GB-00026729.
PR
XX (MEDI-) MEDICAL RES COUNCIL.
PA
XX Rabbitts TH, Tanaka T;
PI
XX WPI; 2004-431946/40.
DR
XX Determining the ability of an immunoglobulin single domain to bind to a
XX target in an intracellular environment by assessing the intracellular
XX interaction between the immunoglobulin domain and the target by
XX monitoring the signal.
XX
XX Disclosure; SEQ ID NO 27; 66pp; English.
XX
XX This invention relates to a novel method of determining the ability of an
XX immunoglobulin single domain to bind to a target in an intracellular
XX environment comprising assessing the intracellular interaction between
XX the immunoglobulin domain and the target by monitoring the signal. The
XX method comprises providing a first molecule and a second molecule, where
XX stable interaction of the first and second molecules leads to the
XX generation of a signal; providing a single intracellular immunoglobulin
XX domain which is associated with the first molecule, where the single
XX immunoglobulin domain is free of complementary immunoglobulin domains;
XX providing an intracellular target which is associated with the second
XX molecule, such that association of the immunoglobulin domain and the
XX target leads to stable interaction of the first and second molecules and
XX generation of the signal; and assessing the intracellular interaction
XX between the immunoglobulin domain and the target by monitoring the
XX signal. The methods are useful for determining the ability of an
XX immunoglobulin single domain to bind to a target in an intracellular
XX environment. The present sequence is that of a single chain variable
XX fragment (scFv) protein which was used to illustrate the method of the
XX invention.
XX
XX SQ Sequence 114 AA;
Query Match 93.2%; Score 550; DB 8; Length 114;
Best Local Similarity 92.9%; Pred. No. 6.2e-39;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
QY 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYVYCOQYVSTPRSGGQVTWEIK 113
Db 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYVYCOQYVSTPRSGGQVTWEIK 113
RESULT 6
ADI26708
ID ADI26708 standard; protein; 122 AA.
XX
XX ADI26708;
AC ADI26708;
XX
XX 15-APR-2004 (first entry)
DT
```

DE Human anti IgM antibody LYM 46 V kappa protein.
XX Human; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW demyelination disease; multiple sclerosis; central nervous system; CNS;
KW axon; glial cell proliferation;
KW Theiler's murine encephalomyelitis virus infection; CNS injury;
KW spinal cord injury.
XX
XX Homo sapiens.
XX US2003185827-A1.
XX 02-OCT-2003.
XX 13-NOV-2001; 2001US-00010729.
XX 29-APR-1994; 94US-00236520.
XX 08-AUG-1996; 96US-00692084.
XX 07-JAN-1997; 97US-00779784.
XX 28-MAY-1999; 99US-00322862.
XX 30-MAY-2000; 2000US-00580787.
XX 05-DEC-2000; 2000US-00730473.
XX (MAYO-) MAYO FOUND.
XX Rodriguez M, Miller DJ, Pease LR;
XX WPI; 2004-119219/12.
XX N-PSDB; ADI26709.
XX New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.
XX
XX Claim 9; Fig 72; 159pp; English.
XX
XX The invention relates to an antibody (I) produced by injecting an
CC immunocompetent host with an antibody peptide, and harvesting the
CC antibody, where the peptide comprises a human anti-IgM antibody fragment
CC given in the specification, or active fragments. Also included are
CC stimulating remyelination of central nervous system (CNS) axons in a
CC mammal (comprising administering a monoclonal antibody, or mixtures,
CC monomers, active fragments, or recombinant antibodies derived from it,
CC characterised by their ability to bind structures and cells within the
CC CNS, including oligodendrocytes), stimulating the proliferation of glial
CC cells in CNS axons in a mammal (comprising administering a monoclonal
CC antibody, or mixtures, monomers, active fragments, or recombinant
CC antibodies derived from it, characterised by their ability to bind
CC structures and cells within the CNS), treating or preventing a
CC demyelinating disease of the CNS in a mammal (comprising administering a
CC monoclonal antibody, or mixtures, monomers, active fragments, or
CC recombinant antibodies derived from it, characterised by their ability to
CC bind structures and cells within the CNS, and to stimulate remyelination
CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
CC cells from mixed cell culture, stimulating remyelination of CNS axons in
CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
CC antibody (or a peptide analogue, hapten, or active fragment of it, where
CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
CC probe capable of screening for the antibody, an assay for screening drugs
CC and other agents for the ability to modulate the production or mimic the
CC activities of mAb sHGM22, sHGM46, or combinations of them, a
CC recombinant virus transformed with recombinant antibody nucleic acids or
CC vector, imaging a portion of the CNS using the antibody and diagnosing or
CC monitoring demyelination and/or remyelination of the CNS comprising using
CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
CC and to stimulate the proliferation of glial cells in CNS axons,
CC optionally in vitro. The antibody is used to treat or prevent a
CC demyelinating disease of the CNS in a human or domestic animal, such as
CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
CC preferably the mammal is a mouse infected with Strain DA of Theiler's
CC murine encephalomyelitis virus. The antibody is used to treat a spinal
CC cord injury and used to screen drugs and other agents for the ability to
CC modulate the production or mimic the activities of the antibody. The

CC antibody can be used to image a portion of the CNS which can be used to
CC diagnose or monitor demyelination and/or remyelination of the CNS. The
CC present sequence is a variable region of a human anti-IgM antibody (or
CC fragment).
XX
XX Sequence 122 AA;
XX
XX Query Match 93.1%; Score 549; DB 8; Length 122;
XX Best Local Similarity 92.0%; Pred. No. 8.1e-39;
XX Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPKLLIYWASTR 60
QY 61 ESGVPAFPFGSGSGDTFTLTINSLOAEDVAVYCCQYVSTPRSGGQGTWVEIK 113
DB 61 ESGVPAFPFGSGSGDTFTLTINSLOAEDVAVYCCQYVSTPRSGGQGTWVEIK 113
RESULT 7
ADF03687
ID ADP03687 standard; protein; 114 AA.
XX
XX ADP03687;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human antibody related protein sequence, SEQ ID 60.
XX
XX Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive;
KW human; antibody; cancer lesion; arteriosclerosis; inflammatory disease;
KW autoimmune disease; cancer.
XX
XX Homo sapiens.
XX
XX WO2004048571-A1.
XX
XX 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-JP014919.
XX
XX 22-NOV-2002; 2002JP-00339241.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
XX (PHAR-) PHARMALOGICALS RES PTE LTD.
XX
XX Tsuchiya M, Suzuki M, Yoshida K, Fujii E, Matsubara K, Tsunoda H;
XX WPI; 2004-450382/42.
XX N-PSDB; ADP03686.
XX
XX Isolating polynucleotide that encodes antibody which acts against
PT lesioned tissue, involves isolating B cells that is infiltrated into
PT lesioned tissue, and acquiring polynucleotide that encodes antibody from
PT isolated B cells.
XX
XX Example 3; SEQ ID NO 60; 200pp; Japanese.
XX
XX The present invention relates to novel antibody sequences, which acts
CC against lesioned tissue. Also claimed is a method (M1) for isolating B
CC polynucleotide encoding the antibodies, which involves (a) isolating B
CC cells that is infiltrated into lesioned tissue, and (b) acquiring
CC polynucleotide that encodes an antibody from the isolated B cells. The
CC antibodies are useful for treating cancer lesions, arteriosclerosis,
CC inflammatory disease or autoimmune disease. The present sequence was used
CC to illustrate the invention.
XX
XX Sequence 114 AA;
XX
XX Query Match 92.5%; Score 546; DB 8; Length 114;
XX Best Local Similarity 92.0%; Pred. No. 1.4e-38;
XX Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
QY 61 ESGVPRFSGSGGTDFTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDFTLTISTLQAEADVAVYCCQYYSTPTPTFGQGTWVEIK 113

RESULT 8
ADP03713
ID ADP03713 standard; protein; 114 AA.
AC ADP03713;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human antibody related protein sequence, SEQ ID 86.
XX
KW Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive;
KW human; antibody; cancer lesion; arteriosclerosis; inflammatory disease;
KW autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN WO2004048571-A1.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-JP014919.
XX
PR 22-NOV-2002; 2002JP-00339241.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PA (PHAR-) PHARMALOGICALS RES PTE LTD.
XX
PI Tsuchiya M, Suzuki M, Yoshida K, Fujii E, Matsubara K, Tsunoda H;
XX
DR WPI; 2004-450382/42.
XX
DR N-PSDB; ADP03712.
XX
PT Isolating polynucleotide that encodes antibody which acts against
PT lesioned tissue, involves isolating B cells that is infiltrated into
PT lesioned tissue, and acquiring polynucleotide that encodes antibody from
PT isolated B cells.
XX
PS Example 4; SEQ ID NO 86; 200pp; Japanese.
XX
CC The present invention relates to novel antibody sequences, which acts
CC against lesioned tissue. Also claimed is a method (M1) for isolating B
CC polynucleotide encoding the antibodies, which involves (a) isolating B
CC cells that is infiltrated into lesioned tissue, and (b) acquiring B
CC polynucleotide that encodes an antibody from the isolated B cells. The
CC antibodies are useful for treating cancer lesions, arteriosclerosis,
CC inflammatory disease or autoimmune disease. The present sequence was used
CC to illustrate the invention.
XX
SQ Sequence 114 AA;
```

```
Query Match 92.5%; Score 546; DB 8; Length 114;
Best Local Similarity 92.0%; Pred. No. 1.4e-38;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
QY 61 ESGVPRFSGSGGTDFTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDFTLTISTLQAEADVAVYCCQYYSTPTPTFGQGTWVEIK 113
```

```
RESULT 9
AAG65565
ID AAG65565 standard; protein; 120 AA.
XX
AC AAG65565;
XX
DT 30-NOV-2001 (first entry)
XX
DE Amino acid sequence of protein seq Id No. 90.
XX
KW Gene library; immunoglobulin; antibody library; human.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-JP001298.
XX
PR 22-FEB-2000; 2000JP-00050543.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
DR WPI; 2001-565420/63.
XX
DR N-PSDB; AAH47729.
XX
PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
PS Examples; p 165; 181pp; Japanese.
XX
CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
SQ Sequence 120 AA;

Query Match 92.5%; Score 546; DB 4; Length 120;
Best Local Similarity 92.0%; Pred. No. 1.4e-38;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
QY 61 ESGVPRFSGSGGTDFTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDFTLTISTLQAEADVAVYCCQYYSTPTPTFGQGTWVEIK 113

RESULT 10
AAB03714
ID AAB03714 standard; protein; 135 AA.
XX
AC AAB03714;
XX
DT 04-OCT-2000 (first entry)
XX
KW Immunoglobulin kappa2 amino acid sequence fragment.
XX
KW Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW immunoglobulin kappa; 19K.
```

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XX OS Unidentified.
XX PN US6048704-A.
XX PD 11-APR-2000.
XX PD 07-MAR-1997; 97US-00812586.
XX PF 07-MAR-1996; 96US-0012976P.
XX PR (UYCO ) UNIV COLUMBIA NEW YORK.
XX PA Trilson MD;
XX PI WPI; 2000-316895/27.
XX DR Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
XX PT disease is purified from human aortic tissue and binds immunoreactively
XX PT with immunoglobulin.
XX PS Example 3; Col 30; 70pp; English.
XX CC The present invention relates to an isolated microfibrillar protein of
XX CC approximately 40kD. The protein is isolated from human aortic tissue and
XX CC binds immunoreactively with immunoglobulin purified from human abdominal
XX CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
XX CC aneurysm-associated antigenic protein (AAAP). The protein is capable of
XX CC forming a disulphide bonded dimer. The protein is immunoreactive with
XX CC human kappa immunoglobulin. Also included in the invention are
XX CC recombinantly produced human AAA proteins. AAAP shows regions of homology
XX CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
XX CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
XX CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
XX CC presence of AAA-associated immunoglobulin bound to the human aortic
XX CC tissue. Antibodies directed against AAAP can be used to detect AAA
XX CC disease. The recombinant protein can be used to induce tolerance to
XX CC antigenic AAA protein in the subject e.g. human. This sequence represents
XX CC an immunoglobulin kappa2 amino acid sequence. The sequence shares
XX CC homology with the AAAP of the invention, it was used to identify and
XX CC characterise AAAP
XX SQ Sequence 135 AA;
Query Match 92.5%; Score 546; DB 3; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.6e-38;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVPA RFSGSGGTDFLTINSIQAEDVAVYQCQYVSTPRSGQGTWVEIK 113
DB 81 ESGVPA RFSGSGGTDFLTINSIQAEDVAVYQCQYVSTPRSGQGTWVEIK 133
RESULT 11
ADA47343
ID ADA47343 standard; protein; 135 AA.
XX AC ADA47343;
XX AC ADA47343;
XX DT 20-NOV-2003 (first entry)
XX DE Human antibody H5IGKAW light chain #SEQ ID 41.
XX KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;
XX KW graft rejection; autoimmune disease; humanised.
XX OS Homo sapiens.
XX PN WO2002102853-A2.
```

```
XX PD 27-DEC-2002.
XX PF 14-JUN-2002; 2002WO-GB002796.
XX XX 14-JUN-2001; 2001GB-00014517.
XX PR 20-SEP-2001; 2001GB-00022724.
XX PR 19-OCT-2001; 2001US-0345194P.
XX PR 18-APR-2002; 2002US-0373470P.
XX PR 18-APR-2002; 2002US-0373471P.
XX XX (ISIS-) ISIS INNOVATION LTD.
XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX PA (TOLE-) TOLERRX INC.
XX XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
XX PI Ringier D, Cobbold S, Winsor-Hines D;
XX XX WPI; 2003-175228/17.
XX DR Treating a primate to induce tolerance to at least one antigen, useful
XX PT for inhibiting graft rejection or treating an autoimmune disease,
XX PT comprises administering a TRX1 antibody to reduce the amount of CD4+
XX PT CD25+ cells produced.
XX PS Example 1; Page 22; 131pp; English.
XX CC The invention relates to a method for treating a primate to induce
XX CC tolerance to at least one antigen. The method of the invention comprises
XX CC administering at least one compound which when in a primary mixed
XX CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells
XX CC produced. The preferred compound is a humanised antibody or its fragment,
XX CC that does not bind to the Fc receptor, and includes CDRs that are free of
XX CC a glycosylation site. The method of the invention is useful for inducing
XX CC tolerance to at least one antigen, specifically for inhibiting,
XX CC ameliorating or reducing an immune response to an antigen. The antibody
XX CC is useful for manufacturing a medicament for inducing tolerance to an
XX CC antigen (possibly in the form of a vaccine), for inhibiting an immune
XX CC response, for inhibiting the rejection of a graft (such as an organ) in a
XX CC human patient, and for treating an autoimmune disease. The current
XX CC sequence represents the human antibody H5IGKAW light chain that was used
XX CC in an example from the invention.
XX SQ Sequence 135 AA;
Query Match 92.5%; Score 546; DB 6; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.6e-38;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVPA RFSGSGGTDFLTINSIQAEDVAVYQCQYVSTPRSGQGTWVEIK 113
DB 81 ESGVPA RFSGSGGTDFLTINSIQAEDVAVYQCQYVSTPRSGQGTWVEIK 133
RESULT 12
ADB72875
ID ADB72875 standard; protein; 135 AA.
XX AC ADB72875;
XX AC ADB72875;
XX DT 04-DEC-2003 (first entry)
XX DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:43.
XX KW Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
XX KW AAA-associated immunoglobulin 40kDa protein.
XX OS Homo sapiens.
XX PN
```

PN US6537769-B1.
 XX
 PD 25-MAR-2003.
 XX
 PF 28-MAR-2000; 2000US-00535832.
 XX
 PR 07-MAR-1996; 96US-0012976P.
 PR 07-MAR-1997; 97US-00812586.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Tilson MD;
 XX
 DR WPI; 2003-687181/65.
 XX
 XX Purified protein useful in diagnosing abdominal aortic aneurysm disease
 PT in subject, e.g. human, contains specified amino acids.
 PT
 XX Disclosure; Col 73-76; 67pp; English.
 XX
 CC The present invention relates to the isolation of a protein approximately
 CC 40kDa which is purified from human aortic tissue. The protein is
 CC immunoreactive with abdominal aortic aneurysms(AAA)-associated
 CC immunoglobulin. The protein is useful for diagnosing AAA disease in a
 CC subject, e.g. human, by administering the protein or a composition
 CC comprising the protein. The inventive protein is capable of forming a
 CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown
 CC function is given in the Sequence Listing but is not mentioned elsewhere
 CC in the specification.
 XX
 XX Sequence 135 AA;
 SQ

 Query Match 92.5%; Score 546; DB 7; Length 135;
 Best Local Similarity 92.9%; Pred. No. 1.6e-38;
 Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

 QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLGWYQKPGQPKLLIYWASTR 60
 DB |||||
 QY 61 ESGVPAFSGSGGTDTLTINSLOAEDVAVYCOQYVSTPRSGGTWVEIK 113
 DB |||||
 DE 81 ESGVDPFSGSGGTDTLTITSSLOAEDVAVYCOQYVSTPPMFGQGTVEIK 133

 RESULT 13
 ADP88458
 ID ADP88458 standard; protein; 135 AA.
 AC ADP88458;
 XX
 XX 09-SEP-2004 (first entry)
 DE Human antibody H5IGKAW VL SEQ ID NO: 35.
 XX
 XX immunosuppressive; transplant rejection; antigen tolerance; antibody;
 KW TRX1; human; H5IGKAW.
 XX
 XX Homo sapiens.
 OS
 XX WO2004052398-A1.
 PN
 XX 24-JUN-2004.
 XX
 XX 09-DEC-2003; 2003WO-US039165.
 PF
 XX 09-DEC-2002; 2002US-0431839P.
 PR
 XX (TOLE-) TOLERRX INC.
 PA
 XX Windsor-Hines D, Rao P, Ringler DJ;
 PI
 XX WPI; 2004-468712/44.
 DR

XX
 PT Treating a primate to induce tolerance to at least one antigen comprises
 PT administering at least one anti-CD4 antibody or its fragment in an
 PT initial dose of at least 40 mg/kg and at least one compound that inhibits
 PT CD8+ T cells.
 XX
 XX Example 1; SEQ ID NO 35; 113pp; English.
 PS
 XX The present invention relates to a process of treating a primate to
 CC induce tolerance to at least one antigen, which comprises administering
 CC to the primate at least one anti-CD4 antibody or its fragment in an
 CC initial dose of at least 40 mg/kg and at least one compound that inhibits
 CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
 CC the primate when the antigen is present in the primate. The method is
 CC useful in treating a primate to induce tolerance to at least one foreign
 CC antigen to prevent transplant rejection. The present sequence is an
 CC antibody fragment used in the exemplification of the invention.
 XX
 XX Sequence 135 AA;
 SQ

 Query Match 92.5%; Score 546; DB 8; Length 135;
 Best Local Similarity 92.9%; Pred. No. 1.6e-38;
 Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

 QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLGWYQKPGQPKLLIYWASTR 60
 DB |||||
 QY 61 ESGVPAFSGSGGTDTLTINSLOAEDVAVYCOQYVSTPRSGGTWVEIK 113
 DB |||||
 DE 81 ESGVDPFSGSGGTDTLTITSSLOAEDVAVYCOQYVSTPPMFGQGTVEIK 133

 RESULT 14
 ADQ87927
 ID ADQ87927 standard; protein; 135 AA.
 XX
 AC ADQ87927;
 XX
 XX 04-NOV-2004 (first entry)
 DT
 XX Human H5IGKAW variable light chain antibody protein.
 DE
 XX Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+;
 KW IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;
 KW antirheumatic; antiarthritic; antidiabetic; neuroprotective;
 KW antiinflammatory; antiallergic; antiasthmatic; cytostatic; antimicrobial;
 KW transplant; graft-versus-host disease; autoimmune disease; inflammation;
 KW allergy; asthma; cancer; infection; human; H5IGKAW.
 XX
 OS Homo sapiens.
 XX
 XX WO2004067554-A2.
 PN
 XX 12-AUG-2004.
 PD
 XX 28-JAN-2004; 2004WO-US002643.
 PF
 XX 29-JAN-2003; 2003US-00353708.
 PR
 XX (TOLE-) TOLERRX INC.
 PA
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
 PI Ringler D, Cobbold S, Winsor-Hines D;
 XX
 XX WPI; 2004-580970/56.
 DR
 XX Inducing tolerance to an antigen comprises administering a CD4 antibody
 PT alone or in combination with other compounds that induce tolerance
 PT against one or more antigens.
 XX

PS Example 1; Page 30; 85pp; English.

XX The invention relates to a novel method for treating a primate to induce

CC tolerance to at least one antigen. The method comprises administering a

CC compound, or a combination of compounds, that induces tolerance against

CC one or more antigens. The compound or the combination being in a primary

CC mixed lymphocyte reaction (MLR) in vitro, which reduces the amount of

CC CD4+ CD25+ cells produced in the mixed lymphocyte reaction and that

CC generates in the primary mixed lymphocyte reaction a cell population that

CC reduces at least one of the amount of CD4+ CD25+ cells produced in vitro

CC in at least one of a primary and secondary mixed lymphocyte reactions,

CC and the amount of at least one of IL-2, IL-4 and IL-12 in a secondary

CC mixed lymphocyte reaction. The compound or the combination being

CC administered in an amount and for a time so as to induce tolerance

CC against the antigen, the compound or the combination being present in the

CC primate when the antigen is present in the primate. The invention further

CC comprises: an antibody that binds to the same epitope as the humanised

CC antibody given in the specification; a composition comprising the

CC antibody and a pharmaceutical carrier; inducing tolerance to an antigen

CC in a patient; inhibiting an immune response in a patient or for

CC inhibiting the rejection of a graft in a human patient; and screening for

CC a compound, or a combination of at least two compounds for use in

CC inducing tolerance. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritic,

CC antidiabetic, neuroprotective, antiinflammatory, antiallergic,

CC antidiarrhetic, cytotatic, and antimicrobial. The composition and methods

CC are useful for inhibiting, preventing or ameliorating an immune response

CC against an antigen, such as in the inhibition or treatment of transplant

CC rejection, graft-versus-host disease, autoimmune diseases (e.g.

CC rheumatoid arthritis, diabetes or multiple sclerosis), inflammation,

CC allergy, asthma, cancer or infections. These may also be used for

CC identifying compounds or agents useful for inducing tolerance against

CC antigens. This sequence represents a human HSIKAW variable light chain

XX antibody protein used in the novel method of the invention.

SQ Sequence 135 AA;

Query Match 92.5%; Score 546; DB 8; Length 135;

Best Local Similarity 92.9%; Pred. No. 1.6e-38;

Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATITCKSSQSIYSSNNKNYLGWYQKQKPPKLLIYWASTR 60

Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSIYSSNNKNYLAWYQKQKPPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGGTDFTLTINSQAEDVAVYCCQYQYVSTPRSFQGTWVEIK 113

Db 81 ESGVPRFSGSGGTDFTLTISLSQAEDVAVYCCQYQYVSTPRSFQGTWVEIK 133

RESULT 15

ADP03811

ID ADP03811 standard; protein; 286 AA.

XX

XX ADP03811;

AC

XX

DT 26-AUG-2004 (first entry)

XX

DE Human antibody related protein sequence, SEQ ID 184.

XX

XX Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive;

KW human; antibody; cancer lesion; arteriosclerosis; inflammatory disease;

KW autoimmune disease; cancer.

XX

OS Homo sapiens.

XX

XX WO2004048571-A1.

PN

XX

PD 10-JUN-2004.

XX

XX 21-NOV-2003; 2003WO-JP014919.

PF

XX

XX 22-NOV-2002; 2002JP-00339241.

PR

XX

XX (CHUS) CHUGAI SEIYAKU KK.

PA (PHAR-) PHARMALOGICALS RES PTE LTD.

XX

PI Tsuchiya M, Suzuki M, Yoshida K, Fujii E, Matsubara K, Tsunoda H;

XX

DR WPI: 2004-450382/42.

DR N-PSDB; ADP03810.

XX

XX Isolating polynucleotide that encodes antibody which acts against

PT lesioned tissue, involves isolating B cells that is infiltrated into

PT lesioned tissue, and acquiring polynucleotide that encodes antibody from

PT isolated B cells.

XX

XX Example 4; SEQ ID NO 184; 200pp; Japanese.

XX

XX The present invention relates to novel antibody sequences, which acts

CC against lesioned tissue. Also claimed is a method (M1) for isolating B

CC polynucleotide encoding the antibodies, which involves (a) isolating B

CC cells that is infiltrated into lesioned tissue, and (b) acquiring B

CC polynucleotide that encodes an antibody from the isolated B cells. The

CC antibodies are useful for treating cancer lesions, arteriosclerosis,

CC inflammatory disease or autoimmune disease. The present sequence was used

CC to illustrate the invention.

XX

SQ Sequence 286 AA;

Query Match 92.5%; Score 546; DB 8; Length 286;

Best Local Similarity 92.0%; Pred. No. 3.4e-38;

Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATITCKSSQSIYSSNNKNYLGWYQKQKPPKLLIYWASTR 60

Db 162 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQKPPKLLIYWASTR 221

Qy 61 ESGVPRFSGSGGTDFTLTINSQAEDVAVYCCQYQYVSTPRSFQGTWVEIK 113

Db 222 ESGVPRFSGSGGTDFTLTISTLQAEDVAVYCCQYQYVSTPRSFQGTWVEIK 274

Search completed: November 16, 2005, 21:51:40

Job time : 66.8088 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.5018 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-22
Perfect score: 590
Sequence: 1 DIVMTQSPDSLAVSLGERAT.....COQYVTPRSGGTWVEIK 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	91.7	113	S34002	Ig kappa chain V r
2	539	91.4	114	K4HULN	Ig kappa chain V-I
3	531	90.0	134	S49531	anti-Sm antibody V
4	530	89.8	129	S40347	Ig kappa chain - h
5	529	89.7	120	S51147	antibody light cha
6	525	89.0	113	S30520	Ig kappa chain V r
7	523	88.6	113	S34003	Ig kappa chain V r
8	522	88.5	134	K4HU17	Ig kappa chain pre
9	517	87.6	113	S30523	Ig kappa chain V r
10	514.5	87.2	133	K4HUJI	Ig kappa chain pre
11	511	86.6	114	S44116	Ig kappa chain V-J
12	508	86.1	114	S44119	Ig kappa chain V-J
13	505	85.6	121	K4HU	Ig kappa chain - h
14	505	85.6	124	S40364	Ig kappa chain pre
15	496.5	84.2	138	A53261	Ig kappa chain pre
16	495	83.9	132	S46373	Ig kappa chain V-J
17	494	83.7	101	PH0869	Ig kappa chain V r
18	487.5	82.6	106	A49138	IgA kappa rheumato
19	480.5	81.4	118	PT0356	Ig kappa chain V r
20	469	79.5	129	S40329	Ig kappa chain V-J
21	469	79.5	134	S21917	Ig kappa chain V r
22	467	79.2	136	A49137	Ig kappa chain pre
23	463	78.5	240	S06084	Ig kappa chain pre
24	461	78.1	102	S43153	Ig kappa chain V-I
25	460	78.0	134	PC1214	Ig kappa chain pre
26	460	78.0	145	PL0014	Ig kappa chain pre
27	459	77.8	113	PL0263	Ig kappa chain V r
28	457.5	77.5	112	S41393	Ig kappa chain V r
29	454	76.9	102	B34153	Ig kappa chain V-I

30 453 76.8 92 2 S37529 Ig kappa chain V r
31 453 76.8 113 2 A49260 antitumor monoclon
32 452 76.6 92 2 S37533 Ig kappa chain V r
33 451.5 76.5 138 2 S26040 Ig kappa chain pre
34 448 75.9 113 2 JC2270 pL7-6 antibody lig
35 447.5 75.8 112 2 S09970 Ig kappa chain V-J
36 447 75.8 92 2 S37532 Ig kappa chain V r
37 447 75.8 92 2 S37534 Ig kappa chain V r
38 446 75.6 92 2 S37535 Ig kappa chain V r
39 444 75.3 92 2 S37530 Ig kappa chain V r
40 444 75.3 214 2 S68212 Ig kappa chain (Ma
41 442.5 75.0 111 2 G30502 Ig kappa chain V r
42 441 74.7 112 2 F30538 Ig kappa chain V r
43 440 74.6 112 2 E30538 Ig kappa chain V r
44 440 74.6 220 2 A31790 Ig kappa chain V r
45 439 74.4 113 2 PL0264 Ig kappa chain V r

ALIGNMENTS

RESULT 1

S34002
IG kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S34002; S30522
R/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:9309281; PMID:7681398
A/Accession: S34002
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <MAR>
A/Cross-references: EMBL:Z18328
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 541; DB 2; Length 113;
Best Local Similarity 91.2%; Pred.No. 1.1e-41;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLIYWASTR 60
QY 61 ESGVPPRFGSGSGTDFTLTINSLQAEADVAVYVYCOQYVTPRSGGTWVEIK 113
DB 61 ESGVPPRFGSGSGTDFTLTISLQAEADVAVYVYCHOYVIGIPRTFGGTVEIK 113

RESULT 2

K4HULN
IG kappa chain V-IV region (Len) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C/Accession: A01903; F61458
R/Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A/Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV v
A/Reference number: A01903; MUID:76004342; PMID:50995
A/Accession: A01903
A/Molecule type: protein
A/Residues: 1-114<SCH>
A/Note: this is the first completely sequenced V region of a new kappa chain subgroup, de
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A/Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso
A/Reference number: A61458; MUID:90039128; PMID:2478651
A/Accession: F61458

```
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This is a Bence Jones protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
F;23-94/Disulfide bonds: #status predicted

Query Match      91.4%; Score 539; DB 1; Length 114;
Best Local Similarity 91.2%; Pred. No. 1.6e-41;
Matches 103; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATICKSSQSYLYSSNNKNYLGWYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPDLSAVSLGERATICKSSQSVLYSSNNKNYLAWSYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 ESGVPARFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPDRFSGSGGTDFTLTISLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C;Accession: S49531
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <WAW>
A;Cross-references: EMBL:X46347; NID:g560841; PIDN:CAA86466.1; PID:g560842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match      90.0%; Score 531; DB 2; Length 134;
Best Local Similarity 90.3%; Pred. No. 1e-40;
Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATICKSSQSYLYSSNNKNYLGWYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIVMTQSPDLSAVSLGERATICKSSQSVLYSSNNKNYLAWSYQKQPPKLLIYWASTR 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 ESGVPARFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 ESGVPDRFSGSGGTDFTLTISLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S40347
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40347
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40347
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-113/Domain: immunoglobulin homology <IMM>
```

```
Query Match      89.8%; Score 530; DB 2; Length 129;
Best Local Similarity 90.2%; Pred. No. 1.2e-40;
Matches 101; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATICKSSQSYLYSSNNKNYLGWYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 DIVMTQSPDLSAVSLGERATICKSSQSVLYSSNNKNYLAWSYQKQPPKLLIYWASTR 77
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 ESGVPARFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 112
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 ESGVPDRFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
S51147
antibody light chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S51147
R;de Kruij, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A;Description: Selection and application of human SCFV antibody fragments from a semi-synthetic library.
A;Reference number: S51147
A;Accession: S51147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <DEK>
A;Cross-references: EMBL:X83714; NID:g633227; PIDN:CAA58689.1; PID:g633228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      89.7%; Score 529; DB 2; Length 120;
Best Local Similarity 90.3%; Pred. No. 1.3e-40;
Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATICKSSQSYLYSSNNKNYLGWYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIELTQSPDLSAVSLGERATICKSSQSVLYSSNNKNYLAWSYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 ESGVPARFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPDRFSGSGGTDFTLTISLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S30520
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S30520
R;Marette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAR>
A;Cross-references: EMBL:Z18325
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      89.0%; Score 525; DB 2; Length 113;
Best Local Similarity 88.5%; Pred. No. 2.9e-40;
Matches 100; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATICKSSQSYLYSSNNKNYLGWYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPDLSAVSLGERATICKSSQSVLYSSNNKNYLAWSYQKQPPKLLIYWASTR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 ESGVPARFSGSGGTDFTLTINSLSQAEADVAVVYCCQYVSTPRSFQGTWVEIK 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Db 61 ESGVPDRFSGSGGTDTTLTISLQAEDVAVYVCOQYNTPLTFGGGTKEIK 113

RESULT 7

S34003

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34003

R:Mariette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34003

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <VAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 523; DB 2; Length 113;

Best Local Similarity 89.4%; Pred. No. 4.4e-40;

Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLGYOQKPGQPPKLLIYWASTR 60

DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLAWYQKAGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTTLTINSLOAEDVAVYVCOQYNTPRSFQGTWVEIK 113

DB 61 ESGVPDRFSGSGGTDTTLTISLQAEDVAVYVCOQYLTPTTFGGGTKEIK 113

RESULT 8

K4HU17

Ig kappa chain precursor V-IV region (B17) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000

C:Accession: A01905

R:Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A:Title: Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.

A:Reference number: A01905; MUID:86041854; PMID:2997713

A:Accession: A01905

A:Molecule type: mRNA

A:Residues: 1-134 <VAR>

A:Note: the sequence was determined from the differentiated gene

A:Note: the authors translated the codon TGC for residue 76 as Trp

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-116/Domain: immunoglobulin homology <IMM>

F:44-60/Region: complementarity-determining 1

F:61-75/Region: framework 2

F:76-82/Region: complementarity-determining 2

F:83-114/Region: framework 3

F:115-121/Region: complementarity-determining 3

F:122-134/Region: framework 4

F:43-114/disulfide bonds: #status predicted

Query Match 88.5%; Score 522; DB 1; Length 134;

Best Local Similarity 90.3%; Pred. No. 6.4e-40;

Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLGYOQKPGQPPKLLIYWASTR 60

DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLAWYQKPGQPPKLLIYCASTR 80

QY 61 ESGVPARFSGSGGTDTTLTINSLOAEDVAVYVCOQYNTPRSFQGTWVEIK 113

DB 81 ESGVPDRFSGSGGTDTTLTISLQAEDVAVYVCOQYNTPLTFGGGTKEIK 133

RESULT 9

S30523

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S30523

R:Mariette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30523

A:Molecule type: mRNA

A:Residues: 1-113 <VAR>

A:Cross-references: EMBL:Z18329

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 517; DB 2; Length 113;

Best Local Similarity 88.5%; Pred. No. 1.5e-39;

Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLGYOQKPGQPPKLLIYWASTR 60

DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLAWYQKAGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTTLTINSLOAEDVAVYVCOQYNTPRSFQGTWVEIK 113

DB 61 ESGVPDRFSGSGGTDTTLTISLQAEDVAVYVCOQYLTPTTFGGGTKEIK 113

RESULT 10

K4HU11

Ig kappa chain precursor V-IV region (J1) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: A01904

R:Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.

Nucleic Acids Res. 13, 6515-6529, 1985

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ line

A:Reference number: A93589; MUID:86041853; PMID:2997712

A:Accession: A01904

A:Molecule type: DNA

A:Residues: 1-133 <KLO>

A:Cross-references: UNIPROT:P06313; GB:Z00022; GB:X51570; NID:G33158; PIDN:CAA77317.1; PDI:1000000000

A:Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV

A:Cross-references: GDB:119341; OMIM:146980

A:Map position: 2p12-2p12

A:Introns: 17/11

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V-IV region (J1) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-116/Domain: immunoglobulin homology <IMM>

F:44-60/Region: complementarity-determining 1

F:61-75/Region: framework 2

F:76-82/Region: complementarity-determining 2

F:83-114/Region: framework 3

F:115-122/Region: complementarity-determining 3

F:123-133/Region: framework 4

F:43-114/disulfide bonds: #status predicted

Query Match 87.2%; Score 514.5; DB 1; Length 133;

Best Local Similarity 89.4%; Pred. No. 3e-39; Mismatches 4; Indels 7; Gaps 1;
Matches 101; Conservative

QY 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
DB 21 DIVWTSQPSDLAVSLGERATIIICKSSQSVLYSSNNKNYLWYQKPGQPPKLLIYWASTR 80
|||||
QY 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113
|||||
DB 81 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 132
|||||

RESULT 11

S44116
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44116
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <HAW>
A/Cross-references: EMBL:Z31391; NID:g472970; PIDN:CAA83266.1; PID:g940527
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 511; DB 2; Length 114;
Best Local Similarity 86.7%; Pred. No. 5.2e-39; Indels 9; Gaps 0;
Matches 98; Conservative

QY 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
DB 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
QY 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113
|||||
DB 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113
|||||

RESULT 12

S44119
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44119
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44119
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <HAW>
A/Cross-references: EMBL:Z31396; NID:g472973; PIDN:CAA83271.1; PID:g940530
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 508; DB 2; Length 114;
Best Local Similarity 87.6%; Pred. No. 9.7e-39; Indels 11; Gaps 0;
Matches 99; Conservative

QY 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
DB 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
QY 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113
|||||

DB 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113
|||||

RESULT 13

K4HU
Ig kappa chain precursor V-IV region - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A01902
R/Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A/Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germli
A/Reference number: A93589; MUID:86041853; PMID:2997712
A/Accession: A01902
A/Molecule type: DNA
A/Residues: 1-121 <KLO>
A/Cross-references: UNIPROT:P06312
A/Note: the sequence was determined from the germline gene
A/Note: there is only one Ig kappa V-IV gene
C/Genetics:

A/Introns: 17/1
A/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>
F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM>
F;44-60/Region: complementarity-determining 1
F;61-75/Region: framework 2
F;76-82/Region: complementarity-determining 2
F;83-114/Region: framework 3
F;115-121/Region: complementarity-determining 3
F;43-114/Disulfide bonds: #status predicted

Query Match 85.6%; Score 505; DB 1; Length 121;
Best Local Similarity 95.0%; Pred. No. 1.9e-38; Indels 3; Gaps 0;
Matches 96; Conservative

QY 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||
DB 21 DIVWTSQPSDLAVSLGERATIIICKSSQSVLYSSNNKNYLWYQKPGQPPKLLIYWASTR 80
|||||

QY 61 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTP 101
|||||
DB 81 ESGVPRFSGSGSGTDTLTINSIQAEDVAVYCCQYVSTP 121
|||||

RESULT 14

S40364
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40364
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:9408091; PMID:8258341
A/Accession: S40364
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-124 <KLE>
A/Cross-references: EMBL:X72474; NID:g441416; PID:g441417
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;26-106/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 505; DB 2; Length 124;
Best Local Similarity 85.8%; Pred. No. 2e-38; Indels 11; Gaps 0;
Matches 97; Conservative

QY 1 DIVWTSQPSDLAVSLGERATIIICKSSQSIYSSNNKNYLWYQKPGQPPKLLIYWASTR 60
|||||

```
Db      11 DIVMTQSPDLSAVSLGERATINCKSRSLYTSNNKNYLAWYQHKFGQPPRLIIYWASNR 70
QY      61 ESGVPARFSGSGGTDFTLTINSLSQAEDEVAVYYCQOYYSTPRSFQGGTWTVEIK 113
Db      71 ESGVPDRFASGSSTGDTFTLTISLSQAEDEVAVYYCQOYYINPISFGGTVKQIK 123
```

RESULT 15

```
A53261
IG kappa chain precursor V-J-C region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C:Accession: A53261
J:Cogne, M.; Freud'homme, J.L.; Bauwens, M.; Touchard, G.; Aucouturier, P.
J. Clin. Invest. 87, 2186-2190, 1991
A:Title: Structure of a monoclonal kappa chain of the Vk-IV subgroup in the kidney and p
A:Reference number: A53261; MUID:91250576; PMID:1904072
A:Accession: A53261
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <COG>
A:Cross-references: GB:M38267
A>Note: authors translated the codon TTG for residue 12 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-116/Domain: immunoglobulin homology <IMM>
```

```
Query Match      84.2%; Score 496.5; DB 2; Length 138;
Best Local Similarity 85.1%; Pred. No. 1.3e-37;
Matches 97; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY      1 DIVMTQSPDLSAVSLGERATINCKSRSLYTSNNKNYLAWYQHKFGQPPRLIIYWASTR 60
Db      21 DIVMTQSPDLSAVSLGERATINCKSLSVFFSPNNKNYLAWYQHKFGQPPRLIIYWASTR 80

QY      61 ESGVPARFSGSGGTDFTLTINSLSQAEDEVAVYYCQOYYST-PRSFQGGTWTVEIK 113
Db      81 ESGVPDRFSGSGGTNFTLTISRQAEDEVAVYYCQOYYTTLSTWTFQGGTVKQIK 134
```

Search completed: November 16, 2005, 22:04:08
Job time : 13.5018 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 63.3548 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-22
Perfect score: 590
Sequence: 1 DIVMTQSPDSLAVSLGERAT.....COQYYSTRPSFGQGTMTVEIK 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	544	92.2	114	1 KV4A_HUMAN	P01625 homo sapien
2	535	90.7	134	1 KV4C_HUMAN	P06314 homo sapien
3	514.5	87.2	133	1 KV4B_HUMAN	P06312 homo sapien
4	505	85.6	121	1 KV40_HUMAN	P83593 homo sapien
5	481	81.5	109	1 KV4D_HUMAN	Q6KB05 mus musculus
6	428	72.5	255	2 Q6KB05	P01605 mus musculus
7	397	67.3	108	1 KV1M_HUMAN	P01667 mus musculus
8	397	67.3	111	1 KV3Q_MOUSE	P01665 mus musculus
9	396	67.1	111	1 KV3M_MOUSE	Q9UL70
10	395	66.9	108	2 Q9UL70	P04207 homo sapien
11	394.5	66.9	129	1 KV3H_HUMAN	P01666 mus musculus
12	394	66.8	111	1 KV3N_MOUSE	P18135 homo sapien
13	393.5	66.7	129	1 KV3L_HUMAN	Q9UL79
14	393	66.6	108	2 Q9UL79	P01624 homo sapien
15	392.5	66.5	109	1 KV3F_HUMAN	P01600 homo sapien
16	391	66.3	108	1 KV1H_HUMAN	P01623 homo sapien
17	390.5	66.2	109	1 KV3E_HUMAN	P01670 mus musculus
18	390	66.1	111	1 KV3R_MOUSE	P01660 mus musculus
19	389	65.9	111	1 KV3H_MOUSE	P01669 mus musculus
20	389	65.9	111	1 KV3Q_MOUSE	Q9UL77
21	386	65.4	108	2 Q9UL77	P01620 homo sapien
22	385.5	65.3	109	1 KV3B_HUMAN	P01673 mus musculus
23	385	65.3	111	1 KV3U_MOUSE	P04431 homo sapien
24	385	65.3	129	1 KV1W_HUMAN	Q66J87 mus musculus
25	384	65.1	238	2 Q66J87	P01622 homo sapien
26	383.5	65.0	109	1 KV3D_HUMAN	P01664 mus musculus
27	383	64.9	111	1 KV3L_MOUSE	Q920E9 mus musculus
28	383	64.9	111	2 Q920E9	P04206 homo sapien
29	382.5	64.8	109	1 KV3G_HUMAN	P18136 homo sapien
30	382.5	64.8	109	2 Q9UL78	
31	382.5	64.8	129	1 KV3M_HUMAN	

32	382	64.7	108	2	Q9UL83	Q9UL83 homo sapien	
33	382	64.7	111	1	KV3S_MOUSE	P01671 mus musculus	
34	381.5	64.7	110	1	KV3P_MOUSE	P01668 mus musculus	
35	381	64.6	236	2	Q6PIT5	Q6PIT5 homo sapien	
36	379.5	64.3	239	2	Q8NEK0	Q8NEK0 homo sapien	
37	378.5	64.2	107	2	Q9ESA9	Q9ESA9 homo sapien	
38	377	63.9	111	1	KV3J_MOUSE	P01662 mus musculus	
39	376.5	63.8	109	2	Q9UL85	Q9UL85 homo sapien	
40	376.5	63.8	117	1	KV2E_HUMAN	P06309 homo sapien	
41	376	63.7	108	1	KV1K_HUMAN	P01603 homo sapien	
42	-	376	63.7	111	1	KV3K_MOUSE	P01663 mus musculus
43	376	63.7	131	1	KV3I_MOUSE	P01661 mus musculus	
44	375	63.6	111	1	KV3T_MOUSE	P01672 mus musculus	
45	375	63.6	236	2	Q6GMW1	Q6GMW1 homo sapien	

ALIGNMENTS

RESULT 1

KV4A_HUMAN

STANDARD;

PRT;

114 AA.

AC

P01625;

DT

21-JUL-1986

(Rel. 01, Created)

DT

01-OCT-1996

(Rel. 34, Last sequence update)

DT

25-OCT-2004

(Rel. 45, Last annotation update)

DE

Ig kappa chain V-IV region Len.

OS

Homo sapiens (Human)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBI_TaxID=9606;

RX

[1]

RP

SEQUENCE.

RP

MEDLINE=76004342; PubMed=50995;

RA

Schneider M., Hilschmann N.;

RT

"The primary structure of a monoclonic immunoglobulin-L-chain of

RL

subgroup IV of the kappa type (Bence-Jones protein Len).";

RL

Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).

RP

[2]

RP

REVISION TO 9.

RA

Salomon A.;

RL

Submitted (AUG-1996) to Swiss-Prot.

CC

-1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

CC

-1- MISCELLANEOUS: This is a Bence-Jones protein.

DR

PDB; 1EQO; X-ray; A/B=1-114.

DR

PDB; 1EEU; X-ray; A/B=1-114.

DR

PDB; 1ERQ; X-ray; A=1-114.

DR

PDB; 1EK3; X-ray; A/B=1-114.

DR

PDB; 1LVE; X-ray; @=1-114.

DR

PDB; 3LVE; X-ray; @=1-114.

DR

PDB; 5LVE; X-ray; A=1-114.

DR

GO; GO:0005576; C:extracellular; NAS.

DR

GO; GO:0003823; F:antigen binding; NAS.

DR

GO; GO:0006955; P:immune response; NAS.

DR

InterPro; IPR007110; IG-like.

DR

InterPro; IPR003596; IG_v.

DR

Pfam; PF00047; ig; 1.

DR

SMART; SM00406; IGV; 1.

DR

PROSITE; PS50835; IG_LIKE; 1.

KW

3D-structure; Bence-Jones protein; Direct protein sequencing;

KW

Immunoglobulin V region.

FT

DOMAIN

1

23

Framework-1.

FT

DOMAIN

24

40

Complementarity-determining-1.

FT

DOMAIN

41

55

Framework-2.

FT

DOMAIN

56

62

Complementarity-determining-2.

FT

DOMAIN

63

94

Framework-3.

FT

DOMAIN

95

101

Complementarity-determining-3.

FT

DOMAIN

102

113

Framework-4.

FT

DISULFID

23

94

By similarity.

FT

STRAND

4

7

FT

STRAND

10

13

FT

TURN

15

16

FT

TURN

19

25

ALIGNMENTS

RESULT 1
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "the primary structure of a monoclonic immunoglobulin-L-chain of
RL Hoppe-Seyley's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR PDB; 1ERQ; X-ray; A/B=1-114.
DR PDB; 1ERU; X-ray; A/B=1-114.
DR PDB; 1ERQ; X-ray; A=1-114.
DR PDB; 1EK3; X-ray; A/B=1-114.
DR PDB; 1LVE; X-ray; @=1-114.
DR PDB; 3LVE; X-ray; @=1-114.
DR PDB; 5LVE; X-ray; A=1-114.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 113
FT DISULFID 23 94
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25


```
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 87.2%; Score 514.5; DB 1; Length 133;
Best Local Similarity 89.4%; Pred. No. 3.1e-45;
Matches 101; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSLYSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQOKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFSGSGGTDTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113
Db 81 ESGVPAFSGSGGTDTLTITSLQAEADVAVYCCQYVSTIP-TFGGTTKVEIK 132

RESULT 4
KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region precursor (fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Abdominal adipose tissue;
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G.; Bornkaun G.W.; Combriato G.; Mocikat R.; Pohlenz H.D.;
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00023; CAA77318.1; -
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
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FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 85.6%; Score 505; DB 1; Length 121;
Best Local Similarity 95.0%; Pred. No. 2.7e-44;
Matches 96; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSLYSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQOKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFSGSGGTDTLTINSLSQAEADVAVYCCQYVSTP 101
Db 81 ESGVPAFSGSGGTDTLTITSLQAEADVAVYCCQYVSTP 121

RESULT 5
KV4D_HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region STH (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E.; Sletten K.; Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 101 Complementarity-determining-3.
FT DOMAIN 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EAE1E12A0B CRC64;

Query Match 81.5%; Score 481; DB 1; Length 109;
Best Local Similarity 86.0%; Pred. No. 7.2e-42;
Matches 92; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSLYSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQOKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFSGSGGTDTLTINSLSQAEADVAVYCCQYVSTPRSGGT 107
Db 61 ESGVPAFSGSGGTDTLTIPGLQAEADVAVYCCQYVRIPTFGG 107

RESULT 6
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Q6KB05
ID Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE ScFv B8E5 Protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; INCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG-Like; 2.
FT NON_TER 1
FT SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 72.5%; Score 428; DB 2; Length 255;
Best Local Similarity 73.5%; Pred. No. 5.6e-36;
Matches 83; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYWASTR 60
Db 137 DIVMAQSPSLVSAGEKVMSCSKSSQSLNSRNQKNYLAWYQKPKQSPKLLIYGASTR 196

Qy 61 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYYSTPRSGFGQGTWVEIK 113
Db 197 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYYSTPRSGFGQGTWVEIK 249

RESULT 7
KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IGM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -1- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human POM V-III kappa chain,
with which it shares certain idiotypic determinants.
CC -1- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
globulin activity.
DR PIR; A01871; K1HULY.
DR HSSP; P01607; LBWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

Pfam: PF00047; ig; 1.
SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-Like; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Complementarity-determining-3.
FT DOMAIN 93 101 Complementarity-determining-4.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111
FT SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 67.3%; Score 397; DB 1; Length 111;
Best Local Similarity 68.1%; Pred. No. 3.5e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYWASTR 60
Db 1 DIVLTQSPASLASLGLGRATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYTASNL 58

Pfam: PF00047; ig; 1.
SMART; SM00406; IGV; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Complementarity-determining-3.
FT DOMAIN 93 101 Complementarity-determining-4.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111
FT SEQUENCE 111 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 67.3%; Score 397; DB 1; Length 108;
Best Local Similarity 67.3%; Pred. No. 3.4e-33;
Matches 76; Conservative 14; Mismatches 17; Indels 6; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYWASTR 60
Db 1 DIVMTQSPSLVSVDGRTITCQASQNV-----NAYLNWYQKPGKGLAPKLLIYGASTR 54

Qy 61 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYYSTPRSGFGQGTWVEIK 113
Db 55 EAGVPSRFPFSGSGSDTFTLTINSLOPEDIATYYCQYNNWPPTFGQGTKEVK 107

RESULT 8
KV3O MOUSE STANDARD; PRT; 111 AA.
ID KV3O_MOUSE
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR PIR; C01937; KVM508.
DR HSSP; P01665; IQNZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-Like; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Complementarity-determining-3.
FT DOMAIN 93 101 Complementarity-determining-4.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111
FT SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 67.3%; Score 397; DB 1; Length 111;
Best Local Similarity 68.1%; Pred. No. 3.5e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYWASTR 60
Db 1 DIVLTQSPASLASLGLGRATIIICKSSQSIYSSNNKYLGYOQKPGQPKLLIYTASNL 58

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QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRFSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 59 ESGIPARFSGSGSGTDTLTNIHPVEEDAATYVCOQSNEDPFTFGSGTKLEIK 111

RESULT 9
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=79073152; PubMed=103003;
RX Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity";
RL Nature 276:785-790(1978).
DR PIR; A01937; KVM543.
DR PDB; 1QNZ; NMR; L=1-111.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFAM; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 67.1%; Score 396; DB 1; Length 111;
Best Local Similarity 68.1%; Pred.No. 4.4e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSQSYLYSSNNKYNLGYOQKPGQPKLLIYWASTR 60
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSYVDYDGD--SYNNWYQOQKPGQPKLLIYAASNL 58

QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRFSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 59 ESGIPARFSGSGSGTDTLTNIHPVEEDAATYVCOQSNEDPFTFGSGTKLEIK 111

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
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RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; LBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 66.9%; Score 395; DB 2; Length 108;
Best Local Similarity 68.1%; Pred.No. 5.5e-33;
Matches 77; Conservative 12; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSQSYLYSSNNKYNLGYOQKPGQPKLLIYWASTR 60
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 DIQMTQSPSSLASVGRVTITCRASQGI-----SNYLAWYQOQKPGKPKSLIYAASLT 54

QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRFSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 55 QSGVPSRFSGSGSGTDTLTISLOPEDVATYVCOQYNSAPRTFGSGTKLEIK 107

RESULT 11
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12740; AAAS8992.1; -.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFAM; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region CLL.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
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FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 118 Complementarity-determining-3.
FT DOMAIN 119 129 JK1 segment.
FT DISULFID 43 108 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 66.9%; Score 394.5; DB 1; Length 129;
Best Local Similarity 70.2%; Pred. No. 7.5e-33;
Matches 80; Conservative 15; Mismatches 12; Indels 7; Gaps 3;

QY 1 DIVVTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPGPKLLIYWASTR 60
DB 21 EIVVTQSPATLSVSPGERATLSQASQSV---SNN---LAWYQKQPGPKLLIYGASTR 74

QY 61 ESGVPAFSGSGGTDFLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 75 ATGIPARFSGSGGTDFLTINSLOAEDVAVYCCQYNNWPPWTFQGTWVEIK 128

RESULT 12
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DE 05-JUL-2004 (Rel. 44, Last sequence update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=79073152; PubMed=103003;
RX Weigert M., Gatmaian L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KWS83.
DR HSSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NCBI_TaxID=10090;
KW Immunoglobulin V region.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 66.8%; Score 394; DB 1; Length 111;
Best Local Similarity 67.3%; Pred. No. 7.2e-33;
Matches 76; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

QY 1 DIVVTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPGPKLLIYWASTR 60
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGD--SYMNWYQKQPGPKLLIYAASNL 58

QY 61 ESGVPAFSGSGGTDFLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 59 ESGIPARFSGSGGTDFLTINHPVEEEDAATYYCQNSNEDPLTFGAGTKLEK 111

RESULT 13
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P10022; K3HUHA.
DR HSSP; P01625; LEEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NCBI_TaxID=9606;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 66.7%; Score 393.5; DB 1; Length 129;
Best Local Similarity 65.5%; Pred. No. 9.6e-33;
Matches 74; Conservative 20; Mismatches 14; Indels 5; Gaps 1;

QY 1 DIVVTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPGPKLLIYWASTR 60
DB 21 EIVLTQSPGTLSPGERATLSQASQSV---SSSYLAWYQKQPGQAPRLIYGASSR 75

QY 61 ESGVPAFSGSGGTDFLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 76 ATGIPDRFSGSGGTDFLTINSLEPEDFAVYCCQYGTSPRTFGQGTWVEIK 128

RESULT 14
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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[1]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR  EMBL; AF035035; AAD56271.1; -.
DR  PIR; S23638; S23638.
DR  PIR; S30521; S30521.
DR  PIR; S34090; S34090.
DR  HSSP; P01607; IEHW.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 66.6%; Score 393; DB 2; Length 108;
Best Local Similarity 68.1%; Pred. No. 8.e-33;
Matches 77; Conservative 11; Mismatches 19; Indels 6; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
QY 61 ESGVPARFSGSGSGTDFTLTINSLSQAEDEVAVYCCQYYSTPRSFSGGTWVEIK 113
Db 56 ATGIPARFSGSGSGTEFTLTISLSQSEDFAVYCCQYYNNMPPPTFGGTRVEIK 108

Search completed: November 16, 2005, 22:01:52
Job time : 63.3548 secs

RESULT 15
KV3P_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RL from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271 (1976).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01897; K3HUPM.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 66.5%; Score 392.5; DB 1; Length 109;
Best Local Similarity 68.1%; Pred. No. 1e-32;
Matches 77; Conservative 16; Mismatches 15; Indels 5; Gaps 1;

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	550	93.2	113	3	US-08-525-539A-80	Sequence 80, Appl
2	549	93.1	114	3	US-09-025-768B-17	Sequence 17, Appl
3	549	93.1	114	4	US-09-490-070A-17	Sequence 17, Appl
4	549	93.1	114	4	US-09-153-17	Sequence 17, Appl
5	549	93.1	114	4	US-09-490-324-17	Sequence 17, Appl
6	546	92.5	135	3	US-08-812-586-46	Sequence 46, Appl
7	546	92.5	135	4	US-09-535-832A-43	Sequence 43, Appl
8	544	92.2	113	4	US-09-274-163E-16	Sequence 16, Appl
9	544	92.2	155	3	US-08-828-741B-11	Sequence 11, Appl
10	544	92.2	155	3	US-09-160-567-11	Sequence 11, Appl
11	544	92.2	155	4	US-09-710-299-11	Sequence 11, Appl
12	544	92.2	155	4	US-09-509-031-11	Sequence 11, Appl
13	544	92.2	342	3	US-08-828-741B-6	Sequence 6, Appl
14	544	92.2	342	3	US-09-160-567-6	Sequence 6, Appl
15	544	92.2	342	4	US-09-710-299-6	Sequence 6, Appl
16	544	92.2	342	4	US-09-509-031-6	Sequence 6, Appl
17	544	92.2	495	3	US-08-828-741B-4	Sequence 4, Appl
18	544	92.2	495	3	US-09-160-567-4	Sequence 4, Appl
19	544	92.2	495	4	US-09-710-299-4	Sequence 4, Appl
20	544	92.2	495	4	US-09-509-031-4	Sequence 4, Appl
21	540	91.5	114	4	US-09-274-163E-2	Sequence 2, Appl
22	540	91.5	114	4	US-09-274-163E-6	Sequence 6, Appl
23	539	91.4	114	1	US-08-360-12S-6	Sequence 6, Appl
24	539	91.4	114	2	US-08-450-578-6	Sequence 6, Appl
25	539	91.4	114	2	US-09-017-628-6	Sequence 6, Appl
26	539	91.4	114	4	US-09-014-880-6	Sequence 6, Appl
27	539	91.4	114	4	US-08-450-363-6	Sequence 6, Appl

Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
QY 61 ESGVPAFSGSGGTDTLTINSLOAEDVAVYYCQYYSTPRSGGTWVEIK 113
Db 61 ESGVDPFRSGSGGTDTLTITSSLOAEDVAVYYCQYYSTPTFGGTWVEIK 113

RESULT 2
US-09-025-769B-17
; Sequence 17, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: protein
; MOLECULE TYPE: protein
US-09-025-769B-17

Query Match 93.1%; Score 549; DB 3; Length 114;
Best Local Similarity 92.9%; Pred. No. 4.9e-47;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFSGSGGTDTLTINSLOAEDVAVYYCQYYSTPRSGGTWVEIK 113
Db 61 ESGVDPFRSGSGGTDTLTITSSLOAEDVAVYYCQYYSTPTFGGTWVEIK 113

RESULT 3
US-09-490-070A-17
; Sequence 17, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim

; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/490,070A
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-070A-17

Query Match 93.1%; Score 549; DB 4; Length 114;
Best Local Similarity 92.9%; Pred. No. 4.9e-47;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFSGSGGTDTLTINSLOAEDVAVYYCQYYSTPRSGGTWVEIK 113
Db 61 ESGVDPFRSGSGGTDTLTITSSLOAEDVAVYYCQYYSTPTFGGTWVEIK 113

RESULT 4
US-09-490-153-17
; Sequence 17, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York


```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match          92.5%; Score 546; DB 3; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.2e-46;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 113
DB 81 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 133

RESULT 7
US-09-535-832A-43
; Sequence 43, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; FILE REFERENCE: Diagnostic and Therapeutic use Thereof
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-43

Query Match          92.5%; Score 546; DB 4; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.2e-46;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 113
DB 81 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 133

RESULT 8
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. 6485943
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match          92.2%; Score 544; DB 4; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.5e-46;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 113
DB 61 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 113

RESULT 9
US-08-828-741B-11
; Sequence 11, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-11

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Best Local Similarity 92.0%; Pred. No. 2.2e-46;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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DB 30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 89

QY 61 ESGVPAFFSGSGGTDFLTINSLOAEDVAVYCCQYISTPRSGQGTWVEIK 113
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US-09-160-567-11
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-No. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-710-299-6

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Best Local Similarity 92.0%; Pred. No. 5.3e-46;
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Db       30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAHYQOKFGQPPKLLIYWASTR 89
         |||||

QY      61 ESGVPARFSGSGGTDFTLTINSQAEDVAVYYCQYYSTPRSFQGTWVEIK 113
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Db       90 ESGVPDRFSGSGGTDFTLTISLSQAEDVAVYYCQYYSTPYSPFGQGTKLEIK 142
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Job time : 20.2142 secs

TEMPERATURE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 69.3787 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-22
Perfect score: 590
Sequence: 1 DIVMTQSPDLSAVSLGERAT.....COQYVSTRPSFGQGTWVEIK 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	590	100.0	113	14	US-10-330-530-22
3	590	100.0	113	16	US-10-660-357-22
4	550	93.2	113	9	US-09-956-206A-80
5	550	93.2	113	18	US-10-965-616-80
6	549	93.1	122	14	US-10-010-729-51
7	548	92.9	114	17	US-10-938-353-112
8	546	92.5	135	14	US-10-171-452A-1
9	546	92.5	135	15	US-10-353-708-1
10	546	92.5	135	16	US-10-731-984-35
11	544	92.2	113	9	US-09-274-163E-16
Sequence 22, Appl					
Sequence 22, Appl					
Sequence 22, Appl					
Sequence 80, Appl					
Sequence 51, Appl					
Sequence 112, Appl					
Sequence 1, Appl					
Sequence 35, Appl					
Sequence 16, Appl					

12	544	92.2	113	18	US-10-880-028-29	Sequence 29, Appl
13	544	92.2	113	18	US-10-880-320-29	Sequence 29, Appl
14	544	92.2	114	17	US-10-700-632-70	Sequence 70, Appl
15	544	92.2	155	14	US-10-345-618-11	Sequence 11, Appl
16	544	92.2	342	14	US-10-345-618-6	Sequence 6, Appl
17	544	92.2	495	14	US-10-345-618-4	Sequence 4, Appl
18	543	92.0	179	17	US-10-644-277-140	Sequence 140, Appl
19	542	91.9	114	20	US-11-031-485-127	Sequence 127, Appl
20	541	91.7	240	9	US-09-799-514-8	Sequence 8, Appl
21	540	91.5	114	9	US-09-274-163E-2	Sequence 2, Appl
22	540	91.5	114	9	US-09-274-163E-6	Sequence 6, Appl
23	540	91.5	119	14	US-10-010-729-13	Sequence 13, Appl
24	540	91.5	264	15	US-10-264-049-4274	Sequence 4274, Ap
25	539	91.4	114	9	US-09-274-163E-4	Sequence 4, Appl
26	539	91.4	114	17	US-10-483-994-8	Sequence 8, Appl
27	539	91.4	114	18	US-10-497-516-8	Sequence 8, Appl
28	539	91.4	114	18	US-10-497-516-8	Sequence 8, Appl
29	538	91.2	114	14	US-10-125-687-11	Sequence 11, Appl
30	538	91.2	114	18	US-10-996-191-11	Sequence 11, Appl
31	535	90.7	113	17	US-10-893-576-174	Sequence 174, Appl
32	535	90.7	133	17	US-10-893-576-26	Sequence 26, Appl
33	534	90.5	113	17	US-10-893-576-173	Sequence 173, Appl
34	534	90.5	133	17	US-10-893-576-36	Sequence 36, Appl
35	533	90.3	163	17	US-10-644-277-100	Sequence 100, Appl
36	533	90.3	220	17	US-10-644-277-20	Sequence 20, Appl
37	532.5	90.3	141	14	US-10-390-986-16	Sequence 16, Appl
38	531	90.0	114	9	US-09-810-502-38	Sequence 38, Appl
39	531	90.0	114	16	US-10-884-133-38	Sequence 38, Appl
40	531	90.0	149	17	US-10-644-277-108	Sequence 108, Appl
41	531	90.0	159	17	US-10-644-277-112	Sequence 112, Appl
42	530	89.8	115	18	US-10-734-661A-88	Sequence 88, Appl
43	530	89.8	163	17	US-10-644-277-12	Sequence 12, Appl
44	530	89.8	211	15	US-10-264-049-4266	Sequence 4266, Ap
45	529	89.7	173	17	US-10-644-277-136	Sequence 136, Appl

ALIGNMENTS

RESULT 1
US-10-330-613-22
; Sequence 22, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-22

Query Match 100.0%; Score 590; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIVMTQSPDLSAVSLGERATII	CKSSQSYLYSSNNKNYLGWYQOKPQPPKLIYWASTR	60
Db	1	DIVMTQSPDLSAVSLGERATII	CKSSQSYLYSSNNKNYLGWYQOKPQPPKLIYWASTR	60
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US-10-330-530-22
; Sequence 22, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-22

Query Match      100.0%; Score 590; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

Qy      61 ESGVPAFSGSGGTDFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
Db      61 ESGVPAFSGSGGTDFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113

RESULT 3
US-10-660-357-22
; Sequence 22, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-22

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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ESGVPAFSGSGGTDFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
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RESULT 4
US-09-956-206A-80
; Sequence 80, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81

US-10-330-530-22
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-956-206A-80

Query Match      93.2%; Score 550; DB 9; Length 113;
Best Local Similarity 92.9%; Pred. No. 7.4e-42;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
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Qy      61 ESGVPAFSGSGGTDFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
Db      61 ESGVPAFSGSGGTDFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113

RESULT 5
US-10-965-616-80
; Sequence 80, Application US/10965616
; Publication No. US20050169915A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/965,616
FILING DATE: 13-Oct-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206
FILING DATE: 17-Sep-2001
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-965-616-80
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Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPKLLIYWASTR 60
QY 61 ESGVPARFSGSGSTDTLTINSLOADQAVYYCQYYSTPRSGQGTMVEIK 113
Db 61 ESGVPDRFSGSGSTDTLTITSLQAEQDAVYYCQYYSTPTFTFGQTKVEIK 113
RESULT 6
US-10-010-729-51
; Sequence 51, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05

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; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-452A-1

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Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEDVAVYCCQYYSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTISLSQAEDVAVYCCQYYSTPPMFGQGTWVEIK 133

RESULT 9
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; Sequence 1, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
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; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-708-1

Query Match          92.5%; Score 546; DB 15; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKPGQPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEDVAVYCCQYYSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTISLSQAEDVAVYCCQYYSTPPMFGQGTWVEIK 133

RESULT 10
US-10-731-984-35
; Sequence 35, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-731-984-35

Query Match          92.5%; Score 546; DB 16; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKPGQPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEDVAVYCCQYYSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTISLSQAEDVAVYCCQYYSTPPMFGQGTWVEIK 133

RESULT 11
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIEFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
```

```
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

Query Match          92.2%; Score 544; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113

RESULT 12
US-10-880-028-29
; Sequence 29, Application US/10880028
; Publication No. US20050163782A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tsung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE OF INVENTION: OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT FILING DATE: 2004-06-28
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-028-29

Query Match          92.2%; Score 544; DB 18; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113

RESULT 13
US-10-880-320-29
; Sequence 29, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tsung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE OF INVENTION: OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT FILING DATE: 2004-06-28
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-028-29

Query Match          92.2%; Score 544; DB 18; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113

RESULT 14
US-10-700-632-70
; Sequence 70, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-70

Query Match          92.2%; Score 544; DB 17; Length 114;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113
```

```
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tsung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE OF INVENTION: OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-29

Query Match          92.2%; Score 544; DB 18; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113

RESULT 14
US-10-700-632-70
; Sequence 70, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-70

Query Match          92.2%; Score 544; DB 17; Length 114;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSYTPRSFGGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTITISLQAEADVAVYCCQYYSYTPSYFGGTWVEIK 113
```

```
RESULT 15
US-10-345-618-11
; Sequence 11, Application US/10345618
; Publication No. US20030148484A1
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/10/345,618
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/509,031
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Kappa
; OTHER INFORMATION: protein sequence
US-10-345-618-11

Query Match          92.2%; Score 544; DB 14; Length 155;
Best Local Similarity 92.0%; Pred. No. 3.5e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db      30 DIVMTSPDSLAVSLGERATINCKSQSILYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89

Qy      61 ESGVPAFFSGSGGTDFTLTINSIQAEDVAVYYCQVYSTPSFGQGTWVEIK 113
Db      90 ESGVPAFFSGSGGTDFTLTINSIQAEDVAVYYCQVYSTPSFGQGTWVEIK 142
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Search completed: November 16, 2005, 23:05:43
Job time : 70.3787 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-26

Perfect score: 562

Sequence: 1 DIQMTQSSSLASVGDVRT.....CQDYDTLPLTFGGTKVIEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	107	7	Adc99797 Anti-huma
2	562	100.0	107	7	Adc99797 Anti-huma
3	562	100.0	107	7	Adc99797 Anti-huma
4	530	94.3	107	8	Adp22412 Human ant
5	527	93.8	108	4	Aau02534 Anti-adip
6	525	93.4	107	2	Aar54319 Anti-HIV
7	525	93.4	107	2	Aaw01287 VL region
8	525	93.4	107	3	Aay98248 Anti-gp12
9	525	93.4	107	3	Aay95139 Anti-gp12
10	523.5	93.1	241	2	Aay21882 Amino aci
11	523	93.1	113	7	Adp28271 Human het
12	523	93.1	152	8	Adk52350 Human het
13	523	93.1	164	7	Adk52350 Human het
14	521	92.7	502	8	Adn97515 Artificia
15	518	92.2	236	8	Adk52378 Monoclon
16	511	91.6	214	8	Adk52358 Human het
17	511	90.9	113	7	Adk52358 Human het
18	511	90.9	164	7	Adk52358 Human het
19	509.5	90.7	238	2	Aay21880 Amino aci
20	506	90.0	107	2	Aaw87455 Humanised
21	505	89.9	272	8	Ado19054 Human ant
22	502	89.3	107	2	Aar54262 Anti-HIV
23	502	89.3	107	2	Aaw01286 VL region
24	502	89.3	107	3	Aay98247 Anti-gp12
25	502	89.3	107	3	Aay95138 Anti-gp12

26	498	88.6	108	4	AAB62785	Aab62785 Human HIV
27	496.5	88.3	106	8	ADP22224	Adp22224 Human ant
28	496	88.3	139	7	ADP90904	Adp90904 Human hep
29	495	88.1	108	8	ADO60452	Ado60452 Human REI
30	494	87.9	108	6	ABO10817	Abol0817 Human ger
31	493	87.7	108	8	ADN41877	Adn41877 Humanised
32	491	87.4	260	5	ABP41164	Abp41164 Human ova
33	487	86.7	107	8	ADR40423	Adr40423 Reshaped
34	487	86.7	107	8	ADR40341	Adr40341 Reshaped
35	487	86.7	120	4	ABG11908	Abg11908 Novel hum
36	486	86.5	107	2	AAR81329	Aar81329 Human REI
37	486	86.5	107	2	AAW86804	Aaw86804 Variable
38	486	86.5	107	2	AAW70623	Aaw70623 Humanised
39	486	86.5	107	2	AAW42275	Aay42275 Human REI
40	486	86.5	107	5	AAU78328	Aau78328 Human REI
41	486	86.5	107	5	ABP61192	Abp61192 Humanised
42	486	86.5	107	6	ABU09373	Abu09373 Light cha
43	486	86.5	107	6	ABU10148	Abu10148 Human REI
44	486	86.5	107	6	ABU62765	Abu62765 Light cha
45	486	86.5	107	7	AAE39071	Aae39071 REI VL pr

ALIGNMENTS

RESULT 1
ADC99797
ID ADC99797 standard; protein; 107 AA.
XX
AC ADC99797;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 26.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; Colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99799.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 3; SEQ ID NO 26; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody

```

CC light chain protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 562; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107

RESULT 2
ADF05401
ID ADD05401 standard; protein; 107 AA.
XX
AC ADD05401;
XX
DT 01-JAN-2004 (first entry)
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 26.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
XX
DR N-PSDB; ADD05403.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
Claim 3; SEQ ID NO 26; 87pp; English.
XX
The invention relates to a novel monoclonal antibody used for inhibiting
XX tumour growth in an animal. The tumour inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumour with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumour. This
XX sequence represents an anti-MUC18 antibody light chain, variable region,
XX protein of the invention.
XX
Sequence 107 AA;
Query Match      100.0%; Score 562; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107

RESULT 3
ADF09839
ID ADF09839 standard; protein; 107 AA.
XX
AC ADF09839;
XX
DT 12-FEB-2004 (first entry)
DE Human anti-MUC18 monoclonal antibody light chain #7.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
XX
DR N-PSDB; ADF09841.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
Claim 3; SEQ ID NO 26; 83pp; English.
XX
The invention comprises a method for inhibiting cell proliferation
XX associated with expression of MUC18 tumour antigen. The method involves
XX administering anti-MUC18 monoclonal antibody. The method of the invention
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX proliferation associated with the expression of MUC18 tumour antigen, the
XX method is preferably useful for inhibiting tumour metastasis. The method
XX is useful for inhibiting cell proliferation in patients with tumours,
XX carcinomas, cancer and other malignancies. The present amino acid
XX sequence represents a light chain from an MUC18 tumour antigen-specific
XX monoclonal antibody.
XX
Sequence 107 AA;
Query Match      100.0%; Score 562; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNWTQKPKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107

```

RESULT 4
ADP22412
ID ADP22412 standard; protein; 107 AA.
XX AC
XX ADP22412;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:318.
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antipoptotic; TNFA antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX OS
XX Homo sapiens.
XX
XX WO2004050683-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038281.
XX
XX 02-DEC-2002; 2002US-0430729P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
XX WPI, 2004-480601/45.
XX
XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
XX Example 10; SEQ ID NO 318; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (1), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFA induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFA induced apoptosis by administering the human monoclonal antibody of
CC (1). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, immunosuppressive, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antipoptotic activities, and can be used
CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC

CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

XX
SQ Sequence 107 AA;

Query Match 94.3%; Score 530; DB 8; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.9e-32;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTSPSSLASVGRVTITTCQASQDINNNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQWTSPSSLASVGRVTITTCQASQDINNNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Qy 61 RFGSGSGDTFTTISGLQPDIAITYCQYDPLTFGSGTKVEIK 107
Db 61 RFGSGSGDTFTTISGLQPDIAITYCQYDPLTFGSGTKLEIK 107

RESULT 5
AAU02534
ID AAU02534 standard; protein; 108 AA.
XX
AC AAU02534;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 22.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
FN W0200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03434.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Claim 1; Page 113-114; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC

CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 108 AA;
Query Match 93.8%; Score 527; DB 4; Length 108;
Best Local Similarity 92.5%; Pred. No. 8.3e-32; Indels 0; Gaps 0;
Matches 99; Conservative 5; Mismatches 3;
QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQLTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
DB 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFGGGKRLK 107
RESULT 6
AAR54319
ID AAR54319 standard; protein; 107 AA.
XX
AC AAR54319;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin light chain variable region B26.
XX
DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
PN WO9407922-A1.
XX
XX 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Example; Page 192; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification

CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XLI Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAb regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54319
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 107 AA;
Query Match 93.4%; Score 525; DB 2; Length 107;
Best Local Similarity 94.3%; Pred. No. 1.2e-31;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 3 QMTQSPSSLSASVGRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPSRF 62
DB 1 EUTQSPSSLSASVGRVTITCOASQDISNHLNWYQKPGKAPKLLIYDASNLETGVPSRF 60
QY 63 SGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
DB 61 SGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFGGGKVEIK 105
RESULT 7
AAR01287
ID AAR01287 standard; protein; 107 AA.
XX
AC AAR01287;
XX
DT 29-JAN-1997 (first entry)
XX
XX VL region of HIV neutralising MAb, clone B26.
XX
DE Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
PN WO9602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
XX


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PS Example; Fig 11; 366pp; English.
CC The sequences given in AAW01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK4 gene
CC clone, B26. A Mab containing this VL sequence has the capacity to reduce
CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC preferentially over the precursor gp160. The Mab may be used for
CC determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX
SQ Sequence 107 AA;

Query Match          93.4%; Score 525; DB 2; Length 107;
Best Local Similarity 94.3%; Pred. No. 1.2e-31;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCASQDINNVLNWKPKGKAPKLLIYDASNLETGVPSPRF 62
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ELTQSPSSLSASVGDRTVITTCASQDISNHLNWKPKGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SSGSGGTDFTTISGLQPEDIAITYCQDYDTLPLTFGGGTKVEIK 107
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SSGSGGTDFTTISGLQPEDIAITYCQDYDTLPLTFGGGTKVEIK 105

RESULT 8
AAV98248
ID AAY98248 standard; protein; 107 AA.
AC AAY98248;
XX
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone b26.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
XX AU9948754-A.
XX
XX 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048754.
XX
PR 16-SEP-1999; 99AU-00048754.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-246867/22.
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AAY98206) and a

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CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
SQ Sequence 107 AA;

Query Match          93.4%; Score 525; DB 3; Length 107;
Best Local Similarity 94.3%; Pred. No. 1.2e-31;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCASQDINNVLNWKPKGKAPKLLIYDASNLETGVPSPRF 62
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ELTQSPSSLSASVGDRTVITTCASQDISNHLNWKPKGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SSGSGGTDFTTISGLQPEDIAITYCQDYDTLPLTFGGGTKVEIK 107
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SSGSGGTDFTTISGLQPEDIAITYCQDYDTLPLTFGGGTKVEIK 105

RESULT 9
AAV95139
ID AAY95139 standard; protein; 107 AA.
AC AAY95139;
XX
XX 30-JUN-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone b26.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Homo sapiens.
XX
XX AU9948756-A.
XX
XX 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-293393/26.
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX Example 9; Fig 11; 366pp; English.
PS

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PR 25-NOV-2002; 2002US-0428807P.
XX (ALEX-) ALEXION PHARM INC..
XX
XX Bowdish KS, Wild MA;
XX WPI; 2003-722327/68.
XX New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX Claim 9; SEQ ID NO 49; 67pp; English.
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody light chain
CC kappa region amino acid sequence, which is used in the exemplification of
CC the present invention.
XX
XX Sequence 113 AA;
Query Match 93.1%; Score 523; DB 7; Length 113;
Best Local Similarity 93.5%; Pred. No. 1.7e-31;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
DB 3 DIQMTSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 62
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 63 RFGSGSGDTFTTISGLQPEDIATYCCQYDNLGVTFGGTKEIK 109
RESULT 12
ADK52350
ID ADK52350 standard; protein; 152 AA.
XX
XX ADK52350;
XX 20-MAY-2004 (first entry)
XX Human anti-MCP-1 variable region light chain #14.
XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
XX Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
XX Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
XX inflammatory condition; cancer; arthritis; multiple sclerosis;
XX anti-MCP-1; heavy chain; light chain.
XX
XX Homo sapiens.
XX
XX WO2004016769-A2.
XX
XX 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US026232.
XX
XX 19-AUG-2002; 2002US-0404802P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas JM, Haak-Frendescho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52349.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
XX Claim 2; SEQ ID NO 56; 154pp; English.
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
XX Sequence 152 AA;
Query Match 93.1%; Score 523; DB 8; Length 152;
Best Local Similarity 92.5%; Pred. No. 2.2e-31;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
DB 1 DIQMTSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDNLPTFGGTKEIK 107
RESULT 13
ADD28243
ID ADD28243 standard; protein; 164 AA.
XX
XX ADD28243;
XX 15-JAN-2004 (first entry)
XX Human heterodimeric antibody light chain kappa region SEQ ID NO:21.
XX human heterodimeric antibody; human; antibody; binding affinity;
XX protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX edema factor; lethal factor; virucide; antibacterial; immunotherapy;
XX anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX Synthetic.
XX Homo sapiens.
XX WO2003076568-A2.
XX
XX 18-SEP-2003.
XX
XX 11-FEB-2003; 2003WO-US004206.
XX
XX 11-FEB-2002; 2002US-0356086P.
XX 29-APR-2002; 2002US-0376408P.
XX 27-SEP-2002; 2002US-0414053P.
XX 25-NOV-2002; 2002US-0428807P.
XX
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Wild MA;
PI

XX WPI; 2003-722327/68.
 XX
 XX New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX
 XX Claim 7; SEQ ID NO 21; 67pp; English.
 XX
 XX The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor (I) has virucide and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
 CC present sequence represents a human heterodimeric antibody light chain
 CC kappa region amino acid sequence, which is used in the exemplification of
 CC the present invention.
 XX
 XX
 XX Sequence 164 AA;
 Query Match 93.1%; Score 523; DB 7; Length 164;
 Best Local Similarity 93.5%; Pred. No. 2.4e-31;
 Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQQKPGKAPKLLIYDASNLETVGPS 60
 Db 3 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQQKPGKAPKLLIYDASNLETVGPS 62
 QY 61 RFSGSGGTFTFTISGLQPEDIATYYCQYDTPLTFTFGGKVEIK 107
 Db 63 RFSGSGGTFTFTISGLQPEDIATYYCQYDNLGVTFGPGTKVDIK 109
 RESULT 14
 ADN97515
 ID ADN97515 standard; protein; 502 AA.
 XX
 XX ADN97515;
 XX
 XX 01-JUL-2004 (first entry)
 XX Artificial protein construction protein #16.
 XX Artificial propeptide; propeptide; protein engineering; antibody.
 XX Unidentified.
 XX WO2004031362-A2.
 XX 15-APR-2004.
 XX 03-OCT-2003; 2003WO-US031420.
 XX 03-OCT-2002; 2002US-0415940P.
 XX (LARG-) LARGE SCALE BIOLOGY CORP.
 XX Reini SJ, Edwards P;
 XX WPI; 2004-330170/30.
 XX N-PSDB; ADN97514.
 XX New artificial propeptide comprises three peptide sequences, useful for
 PT artificial multimeric protein engineering in eukaryotes.
 XX Example 2; SEQ ID NO 88; 244pp; English.
 XX The invention relates to an artificial propeptide comprising three
 CC

CC peptide sequences: a first peptide sequence of interest, a propeptide
 CC sequence attached to the C-terminus of the first peptide sequence of
 CC interest, and a second peptide of interest attached to the C-terminus of
 CC the propeptide sequence. The artificial propeptide and polynucleotides
 CC are useful for artificial multimeric protein engineering, e.g. antibodies
 CC and antibody fragments in eukaryotes. This sequence corresponds to a
 CC protein used in the generation of the protein of the invention.
 XX
 XX Sequence 502 AA;
 Query Match 92.7%; Score 521; DB 8; Length 502;
 Best Local Similarity 92.5%; Pred. No. 9.3e-31;
 Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQQKPGKAPKLLIYDASNLETVGPS 60
 Db 23 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQQKPGKAPKLLIYDASNLETVGPS 82
 QY 61 RFSGSGGTFTFTISGLQPEDIATYYCQYDTPLTFTFGGKVEIK 107
 Db 83 RFSGSGGTFTFTISGLQPEDIATYYCQYDNLPLTFTFGGKVEIK 129
 RESULT 15
 ADD93785
 ID ADD93785 standard; protein; 236 AA.
 XX
 XX ADD93785;
 XX
 XX 29-JAN-2004 (first entry)
 XX Monoclonal antibody 20.13.3 light chain.
 XX Monoclonal antibody; antibody; antiasthmatic; antiallergic;
 KW antiinflammatory; immunosuppressive; dermatological;
 KW gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological;
 KW bronchodilator; interleukin-5; human; gene therapy.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..22 /note= "Signal peptide"
 FT Protein 23..236 /note= "Light chain"
 FT Misc-difference 23..130 /note= "Region specifically described in Claim 2"
 FT Misc-difference 46..119 /note= "Region specifically described in Claim 2"
 FT Region 46..56 /note= "CDR1"
 FT Region 72..78 /note= "CDR2"
 FT Region 111..119 /note= "CDR3"
 XX WO2003085089-A2.
 XX 16-OCT-2003.
 XX 27-MAR-2003; 2003WO-US009260.
 XX 29-MAR-2002; 2002US-0369044P.
 XX (SCHE) SCHERING CORP.
 XX (ABGE-) ABGENIX INC.
 XX Greenfeder S, Corvalan J;
 XX WPI; 2003-804302/75.
 XX N-PSDB; ADD93784.
 XX New antibody or its antigen-binding fragment that specifically binds

PT interleukin-5, useful for diagnosing, treating or preventing a condition
PT associated with undesired interleukin-5 activity, e.g. asthma or allergic
PT rhinitis.

XX
PS
XX
XX
XX
CC

CC The present sequence is the protein sequence of the light chain of anti-
CC human interleukin-5 (IL-5) human monoclonal antibody (MAB) 20.13.3. To
CC obtain this IgG4 MAb, Xenomice (TM) were immunised with human IL-5.
CC Spleen and/or lymph nodes were then fused with myeloma P3-X63-Ag8.653 or
CC myeloma NSO-bcl2 cells, and hybridomas were screened by ELISA for the
CC presence of human IgG/kappa specific for IL-5. Nucleotides comprising the
CC present sequence, or nucleotides 1-707, 1102-1137, 1256-1585, 1683-2002,
CC 58-709, and 148-381 of it, are claimed and used in methods of the
CC invention. The invention relates to antibodies or their antigen-binding
CC fragments that specifically bind IL-5. Human anti-IL-5 antibodies are
CC provided, including chimeric, bispecific, derivatised, single chain
CC antibodies or portions of fusion proteins, and methods of making anti-IL-
CC 5 antibodies, pharmaceutical compositions comprising these antibodies and
CC methods of using the antibodies and compositions for diagnosis and
CC treatment. The invention also provides gene therapy methods using nucleic
CC acids encoding the heavy and/or light chain molecules that comprise the
CC human anti-IL-5 antibodies, and transgenic animals. The antibodies can be
CC used to prevent or inhibit a condition or disorder characterised by
CC undesired IL-5 activity, including asthma, asthma exacerbations, asthma
CC worsening episodes, chronic pneumonia, allergic rhinitis, perennial
CC allergic rhinitis, allergic bronchopulmonary aspergillosis,
CC hyper eosinophilia, Churg-Strauss syndrome, atopic dermatitis, onchocercal
CC dermatitis, episodic angioedema, eosinophilic myalgia syndrome, coeliac
CC disease, eosinophilic gastroenteritis, helminth infections, Hodgkin's
CC disease, nasal polyps, Loeffler's syndrome, urticaria, hyper eosinophilic
CC bronchitis, arteritis nodosa, sinusitis, chronic sinusitis, eosinophilic
CC oesophagitis, allergic eosinophilic oesophagitis, or allergic
CC conjunctivitis, by decreasing or inhibiting the infiltration of
CC eosinophils into affected tissue. The antibodies are also useful for
CC preventing or inhibiting an IL-5 mediated allergic response in a subject
CC or an IL-5 mediated event, such as eosinophil proliferation, maturation,
CC survival, activation, migration into the bloodstream, adhesion to
CC endothelium, infiltration into tissues, pulmonary oedema,
CC bronchoconstriction, airway hyperresponsiveness, pulmonary eosinophilia
CC or neutrophilia, cutaneous eosinophilia, or airway epithelial damage (all
CC claimed).

XX
SQ Sequence 236 AA;

Query Match 92.2%; Score 518; DB 7; Length 236;
Best Local Similarity 93.5%; Pred. No. 7.8e-31;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITCQASQDINNYLNWYQKPKAPKLLIYDASNLETGVPS 60
Db |||||
23 DIQMTQSPSLSASVGRVTITCQASQDINNYLNWYQKPKAPKLLIYDASNLETGVPS 82
QY 61 RFGSGSGDTFTTISGLQPDIAITYCCQYDPLPLTFGGGTVK 107
Db |||||
83 RFGSGSGDTFTTISGLQPDIAITYCCQYDPLPLTFGGGTVK 129

Search completed: November 16, 2005, 21:51:41
Job time : 62.3676 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-26
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDVRT.....CQYDTLPLTFGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522	92.9	129	S52789	Ig kappa chain V r
2	517	92.0	108	K1HUAG	Ig kappa chain V-I
3	515	91.6	110	S44118	Ig kappa chain V-J
4	508	90.4	108	K1HURY	Ig kappa chain V-I
5	505	89.9	108	K1HUAU	Ig kappa chain V-I
6	496	88.3	139	S40365	Ig kappa chain - h
7	490	87.2	108	I39154	Ig kappa chain (BR
8	486	86.5	108	K1HURE	Ig kappa chain V-I
9	485	86.3	117	S42263	Ig kappa chain V r
10	485	86.3	117	S43528	Ig kappa chain V r
11	479	85.2	95	PH0862	Ig kappa chain V r
12	479	85.2	108	S49047	Ig kappa chain V r
13	476	84.7	125	S40349	Ig kappa chain V-J
14	475	84.5	108	K1HULY	Ig kappa chain V-I
15	473	84.2	107	S36264	Ig kappa chain V
16	473	84.2	108	K1HUSW	Ig kappa chain V-I
17	470	83.6	95	PH0864	Ig kappa chain V r
18	470	83.6	124	S40348	Ig kappa chain V-J
19	468	83.3	108	S19674	Ig kappa chain V r
20	465	82.7	123	S40331	Ig kappa chain - h
21	465	82.7	127	S40367	Ig kappa chain V-J
22	464	82.6	129	S52793	Ig kappa chain V r
23	462	82.2	135	S24320	Ig kappa chain pre
24	461	82.0	131	S40352	Ig kappa chain V-J
25	460	81.9	129	S40317	Ig kappa chain - h
26	459	81.7	108	S36279	Ig kappa chain V
27	459	81.7	125	S40333	Ig kappa chain V-J
28	458	81.5	107	S36269	Ig kappa chain V
29	458	81.5	125	S40316	Ig kappa chain - h

30	457	81.3	132	2	S40334	Ig kappa chain - h
31	456	81.1	108	1	K1HUKA	Ig kappa chain V-I
32	456	81.1	125	2	S40353	Ig kappa chain V-J
33	454.5	80.9	107	2	S36275	Ig lambda chain V
34	453	80.6	108	1	K1HUBI	Ig kappa chain V-I
35	452	80.4	108	1	K1HUSW	Ig kappa chain V-I
36	452	80.4	122	2	S40370	Ig kappa chain - h
37	451	80.2	107	2	S36262	Ig lambda chain V
38	451	80.2	122	2	S40314	Ig kappa chain - h
39	451	80.2	129	1	K1HUKW	Ig kappa chain pre
40	449	79.9	109	2	S31998	Ig kappa chain - h
41	449	79.9	109	2	S31981	Ig kappa chain - h
42	448	79.7	108	1	K1HUDE	Ig kappa chain V-I
43	448	79.7	112	1	K1HUNY	Ig kappa chain V-I
44	448	79.7	125	2	S40350	Ig kappa chain - h
45	447	79.5	108	2	S36277	Ig lambda chain V

ALIGNMENTS

RESULT 1

S52789
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52789
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85995; NID:g758598; PIDN:CAAS9987.1; PID:g758599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 522; DB 2; Length 129;
Best Local Similarity 92.5%; Pred. No. 3.6e-38;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDVRTITCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS	60
Db	23	DIQMTQSPSSLSASVGDVRTITCQASQDISNLYNWYQKPGKAPKLLIHAASSLETGVPS	82
QY	61	RFSGSGSGTDFTTTISGLQPEDIATYYCQYDTLPLTFGGGTKVEIK	107
Db	83	RFSGSGSGTDFSTTSSLPQEDLATYYCQYDNLPLTFGGGTKVEIK	129

RESULT 2

K1HUAG
Ig kappa chain V-I region (Ag) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01861
R:Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
A:Reference number: A92047; MUID:69234734; PMID:4893682
A:Accession: A01861
A:Molecule type: protein
A:Residues: 1-108 <TIT>
A:Cross-references: UNIPROT:P01593
A>Note: the sequence of the C region, which has the Inv (3) marker, is also given
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEIK 107
Db 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEIK 107

RESULT 6

Ig kappa chain - human
S40365
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40365
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40365
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:X72475; NID:G441418; PIDN:CAA51143.1; PID:G441419
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 496; DB 2; Length 139;
Best Local Similarity 88.8%; Pred. No. 6.7e-36;
Matches 95; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 16 DIQMTQSPSSLSASVGDRTVITTCQATQDIGNLYNWYQKPGKAPKLLIYDASNLETGVPS 75
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEIK 107
Db 76 RFGSGSGTDFTTISGLQPEDIATYCCQYGNLPTFGPGTKVHK 122

RESULT 7

Ig kappa chain (BRE) - human (fragment)
I39154
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C:Accession: I39154
R:Schormann, N.; Murrell, J.R.; Liepnicks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A:Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A:Reference number: I39154; MUID:96003804; PMID:7568160
A:Accession: I39154
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-108 <RES>
A:Cross-references: EMBL:U31344; NID:G944925; PIDN:AAA79238.1; PID:G944926
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 490; DB 2; Length 108;
Best Local Similarity 88.8%; Pred. No. 1.7e-35;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASTLETGVPS 60
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEIK 107
Db 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEIK 107

RESULT 8

Ig kappa chain V-I region (Rei) - human (tentative sequence)
KIHURE
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A91663; A01873
R:Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A:Title: Die Primärstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom ki
vollstaendige Aminosaeuresequenz des Proteins.
A:Reference number: A91663; MUID:76023758; PMID:809329
A:Accession: A91663
A:Molecule type: Protein
A:Residues: 1-108 <PAL>
A:Cross-references: UNIPROT:P01607
A>Note: the C region of this chain has the Inv (1,2) marker
R:Epp, O.; Lattman, E.B.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A:Title: The molecular structure of a dimer composed of the variable portions of the Ben
A:Reference number: A90392; MUID:76039968; PMID:1182131
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This is a Bence Jones protein.
C:Genetics:

A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapi
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status experimental

Query Match 86.5%; Score 486; DB 1; Length 108;
Best Local Similarity 86.8%; Pred. No. 3.8e-35;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIKLYLNWYQKPGKAPKLLIYEASNLQAGVPS 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDPLPTFGGKTKEI 106
Db 61 RFGSGSGTDFTTISGLQPEDIATYCCQYQSLPYTFQGGTKLQI 106

RESULT 9

Ig kappa chain V region (08) - human
S42263
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42263
R:Scott, M.G.; Crimmings, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SCO>
A:Cross-references: EMBL:M64855; NID:G185963; PIDN:AAA58925.1; PID:G185964
C:Genetics:

A:Introns: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 485; DB 2; Length 117;
Best Local Similarity 96.8%; Pred. No. 5e-35;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNYLNWYQKPGKAPKLLIYDASNLETGVPS 60

Search completed: November 16, 2005, 22:04:09
Job time : 13.7849 secs

Db 61 RFSGSGGTDTLTITSSLOPEDFATVYCCOYSNYPLTFGGGTVKDIK 107

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-26

Perfect score: 562

Sequence: 1 DIQWTQSPSSLSASVGRVT.....CQYDTLPLTGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	92.0	108	1 KV1A_HUMAN	P01593 homo sapien
2	510	90.7	108	1 KV1Y_HUMAN	P80362 homo sapien
3	508	90.4	108	1 KV1P_HUMAN	P01608 homo sapien
4	505	89.9	108	1 KV1B_HUMAN	P01594 homo sapien
5	486	86.5	108	1 KV1O_HUMAN	P01607 homo sapien
6	475	84.5	108	1 KV1M_HUMAN	P01605 homo sapien
7	473	84.2	108	1 KV1Q_HUMAN	P01609 homo sapien
8	468	83.3	236	2 Q6GMX0	Q6gmxx0 homo sapien
9	467.5	83.2	107	2 Q6GSA9	Q96sa9 homo sapien
10	459	81.7	108	2 Q9UL70	Q9ul70 homo sapien
11	456	81.1	108	1 KV1K_HUMAN	P01603 homo sapien
12	453	80.6	108	1 KV1C_HUMAN	P01595 homo sapien
13	453	80.6	236	2 Q723Y4	Q723y4 homo sapien
14	452	80.4	108	1 KV1S_HUMAN	P01611 homo sapien
15	452	80.4	108	2 Q9UL77	Q9ul77 homo sapien
16	452	80.4	236	2 Q6GMX9	Q6gmxx9 homo sapien
17	451	80.2	129	1 KV1W_HUMAN	P04431 homo sapien
18	450	80.1	236	2 Q6GMX8	Q6gmxx8 homo sapien
19	450	80.1	244	2 Q6SZC8	Q6szc8 homo sapien
20	448	79.7	108	1 KV1E_HUMAN	P01597 homo sapien
21	448	79.7	112	1 KV1U_HUMAN	P01613 homo sapien
22	448	79.7	236	2 Q6PIH7	Q6pih7 homo sapien
23	446.5	79.4	107	2 Q9UL81	Q9ul81 homo sapien
24	446	79.4	108	1 KV1V_HUMAN	P04430 homo sapien
25	445	79.2	116	2 Q96PF6	Q96pf6 homo sapien
26	445	79.2	240	2 Q6SZC9	Q6szc9 homo sapien
27	442	78.6	108	1 KV1H_HUMAN	P01600 homo sapien
28	438	77.9	236	2 Q6GMW1	Q6gmw1 homo sapien
29	436	77.6	108	1 KV1F_HUMAN	P01598 homo sapien
30	436	77.6	108	1 KV1R_HUMAN	P01610 homo sapien
31	435	77.4	236	2 Q6PIH4	Q6pih4 homo sapien

ALIGNMENTS

RESULT 1

KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS: Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; K1HUAG.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 92.0%; Score 517; DB 1; Length 108;

Best Local Similarity 92.5%; Pred. No. 2.6e-43;

Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCQASQDINNLYNQKPGKAPKLLIYDASNLTGVPS 60

Db 1 DIQWTQSPSSLSASVGRVTITCQASQDINNLYNQKPGKAPKLLIYDASNLTGVPS 60

Qy 61 RFGSGSGTDTFTTISGLQPDIAIYYCQYDTLPLTGGGKVEIK 107

Db	61	RFSGSGFGDTFTFTISGLQPEDIATYYCQYDTLPRTFGGTKLEIK	107
RESULT 2			
KVIY_HUMAN	STANDARD;	PRT;	108 AA.
ID	KVIY_HUMAN		
AC	P80362;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Ig kappa chain V-I region VAR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).		
RX	MEDLINE=95086080; PubMed=7993911;		
RA	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,		
RA	Solomon A., Stevens F.J., Schiffer M.;		
RT	"Comparison of crystal structures of two homologous proteins:		
RT	Structural origin of altered domain interactions in immunoglobulin		
RT	light-chain dimers.";		
RL	Biochemistry 33:14848-14857(1994).		
RN	[2]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE=81367384; PubMed=6167731;		
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,		
RA	Popp R.A., Solomon A.;		
RT	"Characterization and preliminary crystallographic data on the VL-		
RT	related fragment of the human kappa Bence Jones protein wat.";		
RL	J. Mol. Biol. 147:185-193(1981).		
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PDB; 1WIL; X-ray; A/B=1-108.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
DR	3D-structure; Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	CONFLICT 30 31		
FT	STRAND 4 7		
FT	STRAND 10 13		
FT	TURN 15 16		
FT	TURN 19 25		
FT	TURN 30 31		
FT	STRAND 33 38		
FT	TURN 40 41		
FT	STRAND 45 49		
FT	TURN 50 52		
FT	STRAND 53 54		
FT	TURN 56 57		
FT	TURN 60 61		
FT	STRAND 62 67		
FT	TURN 68 69		
FT	TURN 70 75		
FT	HELIX 80 82		
FT	STRAND 84 90		
FT	STRAND 98 98		
FT	STRAND 102 106		
FT	NON_TER 108 108		
Query Match			
Best Local Similarity 90.4%; Score 508; DB 1; Length 108;			
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;			
QY	1	DIQMTQSPSSLSASVGDRVTITCOASQDINNYLNWYQKPKGKAPKLLIYDASNLETVGVS	60
Db	1	DIQMTQSPSSLSASVGDRVTITCRASQDITNVNWFQRPQGPQAPKVLIVGASILETVGVS	60
QY	61	RFSGSGSGTDFTFTISGLQPEDIATYYCQYDTLPRTFGGTKVEIK	107
Db	61	RFSGSGSGTDFTFTISGLQPEDIATYYCQYDTLPRTFGGTKVDIK	107
RESULT 3			
KVIP_HUMAN	STANDARD;	PRT;	108 AA.
ID	KVIP_HUMAN		
AC	P01608;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Ig kappa chain V-I region Roy.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=68362076; PubMed=5595110;		
RA	Hilschmann N.;		
RT	"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and		
RT	Cum.).";		
RL	Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).		
RN	[2]		
RP	REVIEWS TO 39 AND 41.		
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,		
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;		
RL	(In) Franek F., Shugar D. (eds.);		
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New		
RL	York (1969).		
CC	-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)		
CC	marker.		
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PIR; A91638; KIHURY.		
DR	HSP; P01607; 1BWV.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
DR	Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	NON_TER 108 108		
FT	SEQUENCE 108 AA; FSACEDE5A313DF3A		
CRC64;			
Query Match			
Best Local Similarity 90.7%; Score 508; DB 1; Length 108;			
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;			
QY	1	DIQMTQSPSSLSASVGDRVTITCOASQDINNYLNWYQKPKGKAPKLLIYDASNLETVGVS	60

Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISIFLNWYQQKPKAPKLLIYDASKLEAGVPS 60
QY 61 RFSGSGSDTFTTISGLQPEDIAIYVCOQYDPLPLTFGGGKVEIK 107
Db 61 RFSGSGSDTFTTISGLQPEDIAIYVCOQYDPLPLTFGGGKVEIK 107
RESULT 4
KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RX RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehnammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146 (1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JW5; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67

FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6FB9 CRC64;
Query Match 89.9%; Score 505; DB 1; Length 108;
Best Local Similarity 90.7%; Pred. No. 4e-42;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISIFLNWYQQKPKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISIFLNWYQQKPKAPKLLIYDASNLETGVPS 60
QY 61 RFSGSGSDTFTTISGLQPEDIAIYVCOQYDPLPLTFGGGKVEIK 107
Db 61 RFSGSGSDTFTTISGLQPEDIAIYVCOQYDPLPLTFGGGKVEIK 107
RESULT 5
KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region REI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein REI); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RT Biochemistry 14:4943-4952 (1975).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.


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Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 107
DB 61 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 107

RESULT 8
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.3%; Score 468; DB 2; Length 236;
Best Local Similarity 83.2%; Pred. No. 4.3e-38;
Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
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Db 23 DIQMTQSPSSLSASVGRVTITTCRASQNNNNYQLKPGKAPNLLIYAASSLSQSGVPS 82
QY 61 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 107
DB 83 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 129

RESULT 9
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34085; S34086.
DR HSSP; P01607; LBW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 83.2%; Score 467.5; DB 2; Length 107;
Best Local Similarity 86.1%; Pred. No. 2e-38;
Matches 93; Conservative 6; Mismatches 6; Indels 3; Gaps 2;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRASQSSISYLNMYQKPGKAPKLLIYAASSLSQSGVPS 60
QY 61 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 107
DB 61 RESGSGGTDTFTTISGLQPEDIAATYCCQYDTLPLTFGGGKVEIK 106

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 81.7%; Score 459; DB 2; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.4e-37;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSGISNLYAWYQKPGKPKSLIYAASLTQSGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTTISGLQPEDVATYYCQKNSAPRTFGGTKEIK 107

RESULT 11
KV1C_HUMAN STANDARD; PRT; 108 AA.
ID KV1C_HUMAN
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01869; KIHUKA.
DR HSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Complementarity-determining-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 By similarity.
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBD5A2F4B CRC64;

Query Match 80.6%; Score 453; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 5.5e-37;
Matches 88; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINSLIWTYQKPGKAPKFLIYDAENLEIGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFRSGSGTDFALSISLQPEDFATYYCQYQYNNLYPTFGGTKEIK 107

Query Match 81.1%; Score 456; DB 1; Length 108;
Best Local Similarity 77.6%; Pred. No. 2.8e-37;
Matches 83; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 1 DIQMTQSPSTLSVSGDRVTITCEASQTVLSVLYNWYQKPGKAPKLLIYAASLTQVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTTISVZPZBFATYYCQYQYLDPLPTFGGTKEIK 107

RESULT 12
KV1C_HUMAN STANDARD; PRT; 108 AA.
ID KV1C_HUMAN
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Bi.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT Bi). 3. The complete amino acid sequence and the genetic significance
RT of the variability principles for the mechanism of antibody
RT formation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01863; KIHUBI.
DR HSP; P01607; IBMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Complementarity-determining-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 By similarity.
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 80.6%; Score 453; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 5.5e-37;
Matches 88; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINSLIWTYQKPGKAPKFLIYDAENLEIGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFRSGSGTDFALSISLQPEDFATYYCQYQYNNLYPTFGGTKEIK 107
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RESULT 13
Q723Y4
AC O723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klotner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 80.6%; Score 453; DB 2; Length 236;
Best Local Similarity 80.4%; Pred. No. 1.3e-36;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 23 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 82
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
DB 83 KFGSGSGTDFTTISGLQPEDIATYCCQYKSPYPTFGGTKVEIK 129

RESULT 14
KV15_HUMAN
ID KV15_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; KIHUMS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00447; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
PT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 80.4%; Score 452; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 6.9e-37;
Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
DB 61 RFGSGSGTDFTTISGLQPEDIATYCCQYKSPYPTFGGTKVEIK 107

RESULT 15
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
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RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match      80.4%; Score 452; DB 2; Length 108;
Best Local Similarity 82.2%; Pred. No. 6.9e-37;
Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCAQSDINNYLNWYQKKGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKKGKAPNLLIYAASSLQSGVPS 60

Qy 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQSYSTSWTFGGGTKEIK 107
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Search completed: November 16, 2005, 22:01:53
Job time : 60.9908 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-26
Perfect score: 562
Sequence: 1 DQMTQSPSSLSASVGRVT.....CQYDTLPLTFFGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	93.4	107	1	US-08-276-852-108
2	525	93.4	107	1	US-08-899-575-108
3	525	93.4	107	1	US-08-899-575-108
4	525	93.4	107	5	PCT-US95-08743-108
5	503	89.5	107	2	US-08-318-157B-6
6	503	89.5	107	4	US-09-253-794-6
7	502	89.3	107	1	US-08-276-852-107
8	502	89.3	107	1	US-08-899-575-107
9	502	89.3	107	1	US-08-899-575-107
10	502	89.3	107	5	PCT-US95-08743-107
11	493	87.7	108	3	US-09-025-769B-14
12	493	87.7	108	4	US-09-490-070A-14
13	493	87.7	108	4	US-09-490-153-14
14	493	87.7	108	4	US-09-490-324-14
15	488	86.8	109	3	US-09-157-370-3
16	486	86.5	107	2	US-08-561-521-6
17	486	86.5	107	2	US-08-652-558-34
18	486	86.5	107	3	US-09-025-203-15
19	486	86.5	107	4	US-09-999-021-15
20	486	86.5	107	4	US-09-999-025-15
21	486	86.5	107	4	US-10-040-997-15
22	486	86.5	107	4	US-09-999-040-15
23	486	86.5	107	4	US-09-998-817-15
24	486	86.5	107	5	PCT-US95-01219-6
25	486	86.5	108	2	US-08-070-116A-7
26	486	86.5	108	2	US-08-116-247-9
27	486	86.5	108	4	US-08-557-050-7

28	486	86.5	108	4	US-08-454-899G-100	Sequence 100, Appl
29	486	86.5	108	4	US-09-348-224-9	Sequence 9, Appl
30	486	86.5	111	1	US-08-137-117D-67	Sequence 67, Appl
31	486	86.5	111	2	US-08-436-717-67	Sequence 67, Appl
32	486	86.5	126	1	US-08-137-117D-71	Sequence 71, Appl
33	486	86.5	126	2	US-08-436-717-71	Sequence 71, Appl
34	486	86.5	214	2	US-07-934-373C-39	Sequence 39, Appl
35	486	86.5	214	3	US-08-437-642B-39	Sequence 39, Appl
36	486	86.5	214	5	PCT-US93-07832-39	Sequence 39, Appl
37	484	86.1	109	2	US-07-934-373C-3	Sequence 3, Appl
38	484	86.1	109	3	US-08-437-642B-3	Sequence 3, Appl
39	484	86.1	109	4	US-08-146-206C-3	Sequence 3, Appl
40	484	86.1	109	4	US-09-705-686-3	Sequence 3, Appl
41	484	86.1	109	4	US-09-705-392A-3	Sequence 3, Appl
42	484	86.1	109	4	US-09-705-398-3	Sequence 3, Appl
43	484	86.1	109	5	PCT-US93-07832-3	Sequence 3, Appl
44	483	85.9	107	2	US-07-934-373C-18	Sequence 18, Appl
45	483	85.9	107	3	US-08-437-642B-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-276-852-108
; Sequence 108, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-108

Query Match 93.4%; Score 525; DB 1; Length 107;
 Best Local Similarity 94.3%; Pred. No. 2.9e-42;
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 62
 DB 1 ELTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 107
 DB 61 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 105

RESULT 2
 US-08-899-575-108
 ; Sequence 108, Application US/08899575
 ; Patent No. 5770440
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbas, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,575
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCRI452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-899-575-108

Query Match 93.4%; Score 525; DB 1; Length 107;
 Best Local Similarity 94.3%; Pred. No. 2.9e-42;
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 62
 DB 1 ELTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 107
 DB 61 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 105

RESULT 2
 US-08-899-575-108
 ; Sequence 108, Application US/08899575
 ; Patent No. 5770440
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbas, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,575
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCRI452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-899-575-108

Query Match 93.4%; Score 525; DB 1; Length 107;
 Best Local Similarity 94.3%; Pred. No. 2.9e-42;
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 62
 DB 1 ELTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 107
 DB 61 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 105

RESULT 2
 US-08-899-575-108
 ; Sequence 108, Application US/08899575
 ; Patent No. 5770440
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbas, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,575
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCRI452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-899-575-108

QY 63 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 107
 DB 61 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 105

RESULT 3
 US-08-899-575-108
 ; Sequence 108, Application US/08899575
 ; Patent No. 5804440
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbas, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,575
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCRI452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-899-575-108

Query Match 93.4%; Score 525; DB 1; Length 107;
 Best Local Similarity 94.3%; Pred. No. 2.9e-42;
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 62
 DB 1 ELTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 107
 DB 61 SGSGSGTDFTTISGLQPEDIAITYYCOQYDNLPLTFGGGTKVEIK 105

RESULT 4
 PCT-US95-08743-108
 ; Sequence 108, Application PC/TUS9508743

GENERAL INFORMATION:
 APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08743
 FILING DATE: 11-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 INFORMATION FOR SEQ ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-08743-108

Query Match 93.4%; Score 525; DB 5; Length 107;
 Best Local Similarity 94.3%; Pred. No. 2.9e-42;
 Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QMTQSPSSLSASVGDRTITCOASQDINNNYQKPKAPKLLIYDASNLETGVPSPRF 62
 Db 1 ELTQSPSSLSASVGDRTITCOASQISNHLNYYQKPKAPKLLIYDASNLETGVPSPRF 60
 QY 63 SGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFFGGGKVEIK 107
 Db 61 SGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFFGGGKVEIK 105

RESULT 5
 US-08-318-157B-6
 Sequence 6, Application US/08318157B
 Patent No. 5874540
 GENERAL INFORMATION:
 APPLICANT: HANSEN, Hans J.
 ARMOUR, Kathryn L.
 TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
 TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/318,157B
 FILING DATE: 05-OCT-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: SAXE, Bernhard D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/464
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-253-794-6

LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-318-157B-6
 Query Match 89.5%; Score 503; DB 2; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.4e-40;
 Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTITCOASQDINNNYQKPKAPKLLIYDASNLETGVPSPRF 60
 Db 1 DIQMTQSPSSLSASVGDRTITCOASQDINNNYQKPKAPKLLIYDASNLETGVPSPRF 60
 QY 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFFGGGKVEIK 107
 Db 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFFGGGKVEIK 107
 RESULT 6
 US-09-253-794-6
 Sequence 6, Application US/09253794
 Patent No. 6676924
 GENERAL INFORMATION:
 APPLICANT: HANSEN, Hans J.
 ARMOUR, Kathryn L.
 TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
 TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/253,794
 FILING DATE: 22-Feb-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,157
 FILING DATE: 05-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: SAXE, Bernhard D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/464
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-253-794-6
 Query Match 89.5%; Score 503; DB 4; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.4e-40;
 Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTITCOASQDINNNYQKPKAPKLLIYDASNLETGVPSPRF 60

Db 1 DIQLTQSPSSLSASVGDRTVITTCQASQDIILKYLNNWYQKPGKAPKLLIYEASNLQAGVPS 60
Qy 61 RFSGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTVKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIATYCCQYQSLPYTFGGGTVKVEIK 107

RESULT 7

US-08-276-852-107
; Sequence 107, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-107

Query Match 89.3%; Score 502; DB 1; Length 107;
Best Local Similarity 89.5%; Pred. No. 4.3e-40;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNNWYQKPGKAPKLLIYDASNLETGVPSRF 62
Db 1 ELTQSPSSLSASVGDRTVITTCQASQDIRNLYNNWYQKPGKAPKLLIYDASNSETGVPSRF 60
Qy 63 SGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTVKVEIK 107
Db 61 SGSGSGRDFTTISGLQPEDVATYCCQHQNVPLTFGGGTVKVEIK 105

RESULT 8

US-08-899-575-107
; Sequence 107, Application US/08899575

; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-107

Query Match 89.3%; Score 502; DB 1; Length 107;
Best Local Similarity 89.5%; Pred. No. 4.3e-40;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNNWYQKPGKAPKLLIYDASNLETGVPSRF 62
Db 1 ELTQSPSSLSASVGDRTVITTCQASQDIRNLYNNWYQKPGKAPKLLIYDASNSETGVPSRF 60
Qy 63 SGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTVKVEIK 107
Db 61 SGSGSGRDFTTISGLQPEDVATYCCQHQNVPLTFGGGTVKVEIK 105

RESULT 9

US-08-899-575-107
; Sequence 107, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170


```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-107

Query Match      89.3%; Score 502; DB 1; Length 107;
Best Local Similarity 89.3%; Pred. No. 4.3e-40;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCOASQDINNNLNNYQOKPGKAPKLLIYDASNLTGVPSPRF 62
Db 1 ELTQSPSSLSASVGDRTVITCOASQDINNNLNNYQOKPGKAPKLLIYDASNLTGVPSPRF 60

QY 63 SGGSGGTDFTFTISGLQPEDIATYYCQYDITLPLTFGGGKVEIK 107
Db 61 SGGSGGRDFTFTISLQPEDVATYYCQHQNVPLTFGGGKVEIK 105

RESULT 10
PCT-US95-08743-107
; Sequence 107, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA: US 08/276,852
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
```

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;
;
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-107

Query Match      89.3%; Score 502; DB 5; Length 107;
Best Local Similarity 89.5%; Pred. No. 4.3e-40;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCOASQDINNNLNNYQOKPGKAPKLLIYDASNLTGVPSPRF 62
Db 1 ELTQSPSSLSASVGDRTVITCOASQDINNNLNNYQOKPGKAPKLLIYDASNLTGVPSPRF 60

QY 63 SGGSGGTDFTFTISGLQPEDIATYYCQYDITLPLTFGGGKVEIK 107
Db 61 SGGSGGRDFTFTISLQPEDVATYYCQHQNVPLTFGGGKVEIK 105

RESULT 11
US-09-025-769B-14
; Sequence 14, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-14

Query Match      87.7%; Score 493; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 3e-39;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDINNNLNNYQOKPGKAPKLLIYDASNLTGVPSP 60
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Db 1 DIQWTSPLSASVGRVTITCRASQISNLYNWYQKPGKAPKLLIYAASSIQQSGVPS 60
Qy 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQYYSTPLTFGGGTKEIK 107

RESULT 12

US-09-490-070A-14
; Sequence 14, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490.070A
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-490-070A-14

Query Match 87.7%; Score 493; DB 4; Length 108;
Best Local Similarity 87.9%; Pred. No. 3e-39;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVTITCRASQISNLYNWYQKPGKAPKLLIYAASSIQQSGVPS 60
Db 1 DIQWTSPLSASVGRVTITCRASQISNLYNWYQKPGKAPKLLIYAASSIQQSGVPS 60
Qy 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQYYSTPLTFGGGTKEIK 107

RESULT 13

US-09-490-153-14
; Sequence 14, Application US/09490153

; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490.153
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025.769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-490-153-14

Query Match 87.7%; Score 493; DB 4; Length 108;
Best Local Similarity 87.9%; Pred. No. 3e-39;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVTITCRASQISNLYNWYQKPGKAPKLLIYAASSIQQSGVPS 60
Db 1 DIQWTSPLSASVGRVTITCRASQISNLYNWYQKPGKAPKLLIYAASSIQQSGVPS 60
Qy 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQYYSTPLTFGGGTKEIK 107

RESULT 14

US-09-490-324-14
; Sequence 14, Application US/09490324
; Patent No. 6828422

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA: US/09/490,324
;; APPLICATION NUMBER: US/09/490,324
;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-324-14

Query Match 87.7%; Score 493; DB 4; Length 108;
Best Local Similarity 87.9%; Pred. No. 3e-39;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCOASODINNNLNNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSNLYWYQKPGKAPKLLIYAASLSQSGVPS 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107
Db 61 RFGSGSGTDFTTISGLQPEDFATYCCQYSTPLTFGGGKVEIK 107

RESULT 15
US-09-157-370-3
; Sequence 3, Application US/09157370A
; Patent No. 6282238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-157-370-3

Query Match 86.8%; Score 488; DB 3; Length 109;
Best Local Similarity 87.9%; Pred. No. 9e-39;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCOASODINNNLNNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSNLYWYQKPGKAPKLLIYDASNLETGVPS 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107
Db 61 RFGSGSGTDFTTISGLQPEDFATYCCQYSLPYTFGGGKVEIK 107

Search completed: November 16, 2005, 22:07:21
Job time : 19.1939 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-26
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQYDTLPLTFGGGKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	14	US-10-330-613-26
2	562	100.0	107	14	US-10-330-530-26
3	562	100.0	107	16	US-10-660-357-26
4	530	94.3	107	17	US-10-727-155-318
5	525	93.4	107	14	US-10-016-986-108
6	523	93.1	113	15	US-10-364-743-49
7	523	93.1	113	16	US-10-452-593-49
8	523	93.1	152	17	US-10-644-277-56
9	523	93.1	164	15	US-10-364-743-21
10	523	93.1	164	16	US-10-452-593-21
11	521	92.7	502	16	US-10-679-620-88
					Sequence 26, Appl
					Sequence 26, Appl
					Sequence 26, Appl
					Sequence 318, Appl
					Sequence 108, Appl
					Sequence 49, Appl
					Sequence 49, Appl
					Sequence 56, Appl
					Sequence 21, Appl
					Sequence 21, Appl
					Sequence 88, Appl

12	521	92.7	502	20	US-11-132-143-88	Sequence 88, Appl
13	518	92.2	236	14	US-10-401-344-4	Sequence 4, Appl
14	515	91.6	214	17	US-10-644-277-64	Sequence 64, Appl
15	512.5	91.2	107	20	US-11-031-485-132	Sequence 132, Appl
16	511	90.9	113	15	US-10-364-743-53	Sequence 53, Appl
17	511	90.9	113	16	US-10-452-593-53	Sequence 53, Appl
18	511	90.9	164	15	US-10-364-743-24	Sequence 24, Appl
19	511	90.9	164	16	US-10-452-593-24	Sequence 24, Appl
20	506	90.0	107	14	US-10-223-880-15	Sequence 15, Appl
21	503	89.5	107	9	US-09-253-794-6	Sequence 6, Appl
22	503	89.5	107	16	US-10-680-734-6	Sequence 6, Appl
23	503	89.5	107	17	US-10-755-382-6	Sequence 6, Appl
24	502	89.3	107	14	US-10-016-986-107	Sequence 107, Appl
25	502	89.3	129	17	US-10-893-576-30	Sequence 30, Appl
26	499	88.8	238	20	US-11-031-485-48	Sequence 48, Appl
27	497	88.4	236	20	US-11-131-648-20	Sequence 20, Appl
28	497	88.4	236	20	US-11-131-648-49	Sequence 49, Appl
29	496.5	88.3	106	17	US-10-727-155-130	Sequence 130, Appl
30	495	88.1	108	16	US-10-307-276B-13	Sequence 13, Appl
31	495	88.1	108	20	US-11-061-956-13	Sequence 13, Appl
32	493	87.7	108	18	US-10-683-815-19	Sequence 19, Appl
33	493	87.4	107	17	US-10-893-576-180	Sequence 180, Appl
34	491	87.4	260	15	US-10-264-049-2296	Sequence 2296, Appl
35	487	86.7	120	18	US-10-450-763-42267	Sequence 42267, Appl
36	486	86.5	107	9	US-09-056-160B-13	Sequence 13, Appl
37	486	86.5	107	9	US-09-999-025-15	Sequence 15, Appl
38	486	86.5	107	9	US-09-999-040-15	Sequence 15, Appl
39	486	86.5	107	10	US-09-998-817-15	Sequence 15, Appl
40	486	86.5	107	10	US-09-999-021-15	Sequence 15, Appl
41	486	86.5	107	14	US-10-040-997-15	Sequence 15, Appl
42	486	86.5	107	14	US-10-234-671-13	Sequence 13, Appl
43	486	86.5	107	15	US-10-366-709-44	Sequence 44, Appl
44	486	86.5	107	17	US-10-763-424-56	Sequence 56, Appl
45	486	86.5	107	17	US-10-974-591-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-330-613-26
; Sequence 26, Application US/10330613
; Publication No. US20030147805A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-26

Query Match 100.0%; Score 562; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLTGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPGKAPKLLIYDASNLTGVPS	60
QY	61	RFGSGSGGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK	107
Db	61	RFGSGSGGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK	107

RESULT 2

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US-10-330-530-26
; Sequence 26, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-26

Query Match      100.0%; Score 562; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 3
US-10-660-357-26
; Sequence 26, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-26

Query Match      100.0%; Score 562; DB 16; Length 107;
Best Local Similarity 100.8%; Pred. No. 1.5e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 4
US-10-727-155-318
; Sequence 318, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock

```

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; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Poord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-318

Query Match      94.3%; Score 530; DB 17; Length 107;
Best Local Similarity 93.5%; Pred. No. 1e-39;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 5
US-10-016-986-108
; Sequence 108, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-108

Query Match          93.4%; Score 525; DB 14; Length 107;
Best Local Similarity 94.3%; Pred. No. 2.9e-39;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTTITCOASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ELTQSPSSLSASVGDRTTITCOASQDISNHLNWNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 63 SSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 105

RESULT 6
US-10-364-743-49
; Sequence 49, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 113
; TYPE: PRT
; ORGANISM: human
US-10-364-743-49

Query Match          93.1%; Score 523; DB 15; Length 113;
Best Local Similarity 93.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTITCOASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 DIQMTQSPSSLSASVGDRTTITCOASQDISNLYNWNQKPGKAPKLLIYDASNLETGVPSPRF 62

QY 61 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 109

RESULT 7
US-10-452-593-49
; Sequence 49, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408

Query Match          93.1%; Score 523; DB 15; Length 113;
Best Local Similarity 93.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTITCOASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 DIQMTQSPSSLSASVGDRTTITCOASQDISNLYNWNQKPGKAPKLLIYDASNLETGVPSPRF 62

QY 61 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 109

RESULT 8
US-10-644-277-56
; Sequence 56, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091a
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-56

Query Match          93.1%; Score 523; DB 17; Length 152;
Best Local Similarity 92.5%; Pred. No. 6.3e-39;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTITCOASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRTTITCOASQDITTYLNNWNQKPGKAPKLLIYDASNLETGVPSPRF 60

QY 61 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGKVEIK 107

RESULT 9
US-10-364-743-21
; Sequence 21, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
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; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 164
; TYPE: PRT
; ORGANISM: human
; US-10-364-743-21

Query Match          93.1%; Score 523; DB 15; Length 164;
Best Local Similarity 93.5%; Pred. No. 6.8e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 3 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 62

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
Db 63 RFGSGSGTDTFTTISGLQPEDIATYCCQYDNLGVTFGGTKVDIK 109

RESULT 10
US-10-452-593-21
; Sequence 21, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 164
; TYPE: PRT
; ORGANISM: human
; US-10-452-593-21

Query Match          93.1%; Score 523; DB 16; Length 164;
Best Local Similarity 93.5%; Pred. No. 6.8e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 3 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 62

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
Db 63 RFGSGSGTDTFTTISGLQPEDIATYCCQYDNLGVTFGGTKVDIK 109

RESULT 11
US-10-679-620-88
; Sequence 88, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reintl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hufab H2 , see Example 2
; NAME/KEY: misc feature
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-11-132-143-88

Query Match          92.7%; Score 521; DB 20; Length 502;
Best Local Similarity 92.5%; Pred. No. 3.3e-38;
Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 23 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 82

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
Db 83 RFGSGSGTDTFTTISGLQPEDFATYCCQYDNLPLTFGGTKVEIK 129

RESULT 12
US-11-132-143-88
; Sequence 88, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reintl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hufab H2 , see Example 2
; NAME/KEY: misc feature
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-11-132-143-88

Query Match          92.7%; Score 521; DB 20; Length 502;
Best Local Similarity 92.5%; Pred. No. 3.3e-38;
Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
```



```

Db      23 DIQMTQSPSSLSASVGDRVTITTCQASQDISNYLNWTHQPKAPKLLIYDASNLETGVPS 82
      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
      83 RFGSGYSGTDFTTISGLQPEDPATYYCQYDNLPLTFGGGKVEIK 129

RESULT 13
US-10-401-344-4
; Sequence 4, Application US/10401344
; Publication No. US20030194404A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Greenfeder, Scott
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME
; TITLE OF INVENTION: COMPRISING SAME
; FILE REFERENCE: LI01564W1
; CURRENT APPLICATION NUMBER: US/10/401,344
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Signal Peptide
; LOCATION: (1)-(22)
; OTHER INFORMATION:
US-10-401-344-4

Query Match          92.2%; Score 518; DB 14; Length 236;
Best Local Similarity 93.5%; Pred. No. 2.8e-38;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 60
Db      23 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 82
QY      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
Db      83 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLHPLTFGGGKVEIR 129

RESULT 14
US-10-644-277-64
; Sequence 64, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-64

Query Match          91.6%; Score 515; DB 17; Length 214;
```

```

Best Local Similarity 90.7%; Pred. No. 4.6e-38;
Matches 97; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 60
Db      1 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 60
QY      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
Db      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLITFGGGRLEIK 107

RESULT 15
US-11-031-485-132
; Sequence 132, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MadCAM
; FILE REFERENCE: ABX-PR6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 132
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-132

Query Match          91.2%; Score 512.5; DB 20; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.8e-38;
Matches 99; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY      1 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 60
Db      1 DIQMTQSPSSLSASVGDRVTITTCQASQDINNLYNWYQKPKAPKLLIYDASNLETGVPS 60
QY      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
Db      61 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLITFGGGRLEIK 106

Search completed: November 16, 2005, 23:05:44
Job time : 66.6949 secs
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-30
Perfect score: 556
Sequence: 1 DQMTQSPSSLSASVGRVT.....CKFSSPPTFGTGKVDIS 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	7	Adc99801 Anti-huma
2	556	100.0	107	7	Add05405 Anti-MUC1
3	556	100.0	107	7	Adf09843 Human ant
4	520	93.5	107	8	Adp22400 Human ant
5	520	93.5	108	8	Adp46984 Murine li
6	520	93.5	242	5	Aau90902 Insulin/i
7	520	93.5	245	5	Aau90947 Insulin/i
8	508	91.4	107	8	Adp22358 Human ant
9	505	90.8	107	7	Adk18922 Anti-huma
10	503	90.5	108	8	Adp46980 Murine li
11	503	90.5	108	8	Adp46982 Murine li
12	503	90.5	239	5	Aau90905 Insulin/i
13	502	90.3	242	5	Aau90904 Insulin/i
14	501	90.1	107	7	Adk18799 Anti-huma
15	501	90.1	107	7	Adk18833 Anti-huma
16	501	90.1	107	8	Adk18608 Anti-huma
17	501	90.1	107	8	Adj57622 TNFa1pha
18	501	90.1	107	8	Adj58753 Human 2SD
19	501	90.1	107	8	Adl25434 Human mAb
20	501	90.1	244	5	ABP44153 Human Bly
21	501	90.1	244	5	ABP44250 Human Bly
22	501	90.1	244	5	ABP44071 Human Bly
23	501	90.1	244	7	ADG94898 Single ch
24	501	90.1	244	7	ADG94980 Single ch
25	501	90.1	244	7	ADG95077 Single ch

ALIGNMENTS

RESULT 1

Adc99801
ID Adc99801 standard; protein; 107 AA.

XX Adc99801;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 30.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; Adc99803.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.

XX Claim 3; SEQ ID NO 30; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
a heavy or light chain amino acid or a heavy or light chain variable
domain where the antibody binds to MUC18. The monoclonal antibody of the
invention demonstrates cytostatic activity and may be useful for treating
a disease or condition associated with the expression of MUC18 on the
cell surface such as tumours, specifically melanoma, oesophageal,
pancreatic or colorectal tumours, carcinomas, particularly cervical
carcinomas and cervical intraepithelial neoplasia and cancers including
colorectal, breast or lung cancer, as well as other malignancies. The
current sequence is that of the anti-human MUC18 monoclonal antibody

```

CC light chain protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 2
AD05405
ID ADD05405 standard; protein; 107 AA.
XX
AC ADD05405;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 30.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN W02003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
XX
N-PSDB; ADD05407.

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
treating tumors, inhibiting tumor growth, inhibiting cell invasion
associated with melanoma, or increasing survival of an animal having a
metastatic tumor.

Claim 3; SEQ ID NO 30; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting
tumor growth in an animal. The tumour inhibition process comprises
selecting an animal in need of treatment for a tumour, providing a
monoclonal antibody comprising a heavy chain amino acid, where the
antibody consists of any one of 10 fully defined sequences of 117-123
amino acids given in the specification, and where the monoclonal antibody
binds MUC18, and contacting the tumour with the antibody resulting in
inhibited proliferation of the cells. The monoclonal antibody has
cytostatic and can be used in the production of a vaccine. The monoclonal
antibodies against the MUC18 antigen are useful for diagnosing and
treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
tumour metastasis), inhibiting cell invasion associated with melanoma, or
increasing survival of an animal having a metastatic tumour. This
sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 3
AD09843
ID ADF09843 standard; protein; 107 AA.
XX
AC ADF09843;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #8.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN W02003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
XX
N-PSDB; ADF09845.

Inhibiting cell proliferation associated with expression of MUC18 tumour
antigen, involves incubating and inhibiting cell by administering anti-
MUC18 monoclonal antibody.

Claim 3; SEQ ID NO 30; 83pp; English.

The invention comprises a method for inhibiting cell proliferation
associated with expression of MUC18 tumour antigen. The method involves
administering anti-MUC18 monoclonal antibody. The method of the invention
is useful for inhibiting cell (e.g. melanoma or tumour cell)
proliferation associated with the expression of MUC18 tumour antigen, the
method is preferably useful for inhibiting tumour metastasis. The method
is useful for inhibiting cell proliferation in patients with tumours,
carcinomas, cancer and other malignancies. The present amino acid
sequence represents a light chain from an MUC18 tumour antigen-specific
monoclonal antibody.

Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFLTITISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107

```

RESULT 4

ADP22400
 ID ADP22400 standard; protein; 107 AA.
 XX
 AC ADP22400;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFa antibody light chain variable region SEQ ID NO:306.
 XX
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang M, Lee R;
 PI Manchulenchon K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX
 DR WPI; 2004-480601/45.
 XX
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 306; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFa
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 107 AA;

Query Match 93.5%; Score 520; DB 8; Length 107;
 Best Local Similarity 94.3%; Pred No. 2,1e-29;
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQQNPVKLLIYGASTLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQQNPVKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPFTFGPGTKVDI 106

Db 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPFTFGPGTKVDI 106

RESULT 5

ADP46984
 ID ADP46984 standard; protein; 108 AA.

XX
 AC ADP46984;

DT 09-SEP-2004 (first entry)

DE Murine light chain variable anti-amphetamine antibody protein SeqID 40.
 KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
 KW PCP; drug addiction; antiaddictive; antibody therapy.

OS Mus musculus.

PN WO2004050032-A2.

PD 17-JUN-2004.

PF 02-DEC-2003; 2003WO-US038384.

PR 02-DEC-2002; 2002US-0430717P.

PA (ABGE-) ABGENIX INC.

XX Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
 PI Feng X;

DR WPI; 2004-460981/43.

XX New isolated antibody or its binding fragment that binds specifically to
 PT a drug of abuse, useful for treating a patient suffering from addiction
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.

PS Example 1; SEQ ID NO 40; 88pp; English.

XX This invention relates to novel antibodies, or binding fragments thereof,
 CC that bind directly to various drugs of abuse. Specifically, it refers to
 CC human or chimeric monoclonal antibodies that are capable of binding to
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present
 CC invention describes generating hybridoma cell lines that produce such
 CC antibodies and transforming a cell with a gene encoding the antibody,
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can
 CC be used to treat a patient suffering from a drug addiction. Accordingly,
 CC these compositions exhibit antiaddictive activities and can be used for
 CC antibody therapy to treat patients suffering from a drug addiction. This
 CC polypeptide sequence is a murine light chain variable anti-amphetamine
 CC antibody of the invention.

XX Sequence 108 AA;

Query Match 93.5%; Score 520; DB 8; Length 108;
 Best Local Similarity 94.3%; Pred. No. 2.1e-29;
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYAASLQSGVPS 60
 QY 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
 DB 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106

RESULT 6
 AAU90902
 ID AAU90902 standard; protein; 242 AA.
 AC AAU90902;
 XX
 XX 18-JUN-2002 (first entry)
 XX Insulin/insulin-like growth factor receptor-binding peptide #2858.
 DE Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 OS Synthetic.
 XX WO200172771-A2.
 PN 04-OCT-2001.
 PD 29-MAR-2000; 2000WO-US008528.
 PF 29-MAR-2000; 2000WO-US008528.
 PR (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX WPI; 2002-025774/03.
 DR Modulating insulin activity in mammalian cells, for treating e.g.
 XX diabetes and tumors, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors.
 XX Example 5; Fig 36; 390pp; English.
 PS The invention relates to a method of modulating insulin activity in
 XX mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the
 CC invention

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYAASLQSGVPS 60
 QY 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
 DB 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106

Query Match 93.5%; Score 520; DB 5; Length 242;
 Best Local Similarity 94.3%; Pred. No. 4.2e-29;

Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 136 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYAASLQSGVPS 195
 QY 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
 DB 196 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 241

RESULT 7
 AAU90947
 ID AAU90947 standard; protein; 245 AA.
 XX
 AC AAU90947;
 XX
 XX 18-JUN-2002 (first entry)
 XX Insulin/insulin-like growth factor receptor-binding peptide #2903.
 DE Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 OS Synthetic.
 XX WO200172771-A2.
 PN 04-OCT-2001.
 PD 29-MAR-2000; 2000WO-US008528.
 PF 29-MAR-2000; 2000WO-US008528.
 PR (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX WPI; 2002-025774/03.
 DR Modulating insulin activity in mammalian cells, for treating e.g.
 XX diabetes and tumors, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors.
 XX Disclosure; Fig 57; 390pp; English.
 PS The invention relates to a method of modulating insulin activity in
 XX mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the
 CC invention

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPGKVPKLLIYAASLQSGVPS 195
 QY 61 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
 DB 196 RFSGSGSGDTFTLTSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 241

Query Match 93.5%; Score 520; DB 5; Length 245;
 Best Local Similarity 94.3%; Pred. No. 4.3e-29;
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 139 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLLIYAASLTQSGVPS 198
 QY 61 RFSGSGSGTDFTLTSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106
 Db 199 RFSGSGSGTDFTLTSSLPEDVATYYCQKFSPPPTFGPGTKVDI 244

RESULT 8
 ADP22358
 ID ADP22358 standard; protein; 107 AA.
 AC ADP22358;
 XX
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFA antibody light chain variable region SEQ ID NO:264.
 DE
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 XX Homo sapiens.
 OS
 PN WO2004050683-A2.
 XX
 XX 17-JUN-2004.
 PD
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanasami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX
 DR WPI; 2004-480601/45.
 DR N-PSDB; ADP22357.
 XX
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 264; 213pp; English.

The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFA induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,

CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 107 AA;
 SQ

Query Match 91.4%; Score 508; DB 8; Length 107;
 Best Local Similarity 91.5%; Pred. No. 1.5e-28;
 Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLLIYAASLTQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLLIYAASLTQSGVPS 60
 QY 61 RFSGSGSGTDFTLTSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106
 Db 61 RFSGSGSGTDFTLTSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106

RESULT 9
 ADK18922
 ID ADK18922 standard; protein; 107 AA.
 XX
 AC ADK18922;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody protein related sequence #148.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen P, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 PT New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 346; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when

CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX
 SQ Sequence 107 AA;

Query Match 90.8%; Score 505; DB 7; Length 107;
 Best Local Similarity 92.5%; Pred. No. 2.4e-28;
 Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106
 DB 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106

RESULT 10
 ADP46980
 ID ADP46980 standard; protein; 108 AA.
 XX
 AC ADP46980;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Murine light chain variable anti-amphetamine antibody protein SeqID 36.
 XX
 KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
 KW PCP; drug addiction; antiaddictive; antibody therapy.
 XX
 OS Mus musculus.
 XX
 PN WO2004050032-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038384.
 PR 02-DEC-2002; 2002US-0430717P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
 PI Feng X;
 XX
 DR WPI; 2004-460981/43.
 XX
 PT New isolated antibody or its binding fragment that binds specifically to
 PT a drug of abuse, useful for treating a patient suffering from addiction
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 XX
 PS Example 1; SEQ ID NO 36; 88pp; English.
 XX
 CC This invention relates to novel antibodies, or binding fragments thereof,
 CC that bind directly to various drugs of abuse. Specifically, it refers to
 CC human or chimeric monoclonal antibodies that are capable of binding to
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present
 CC invention describes generating hybridoma cell lines that produce such
 CC antibodies and transforming a cell with a gene encoding the antibody,
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can
 CC be used to treat a patient suffering from a drug addiction. Accordingly,
 CC these compositions exhibit antiaddictive activities and can be used for
 CC antibody therapy to treat patients suffering from a drug addiction. This
 CC polypeptide sequence is a murine light chain variable anti-amphetamine
 CC antibody of the invention.
 XX
 SQ Sequence 108 AA;

Query Match 90.5%; Score 503; DB 8; Length 108;
 Best Local Similarity 91.5%; Pred. No. 3.3e-28;
 Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106
 DB 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106

RESULT 11
 ADP46982
 ID ADP46982 standard; protein; 108 AA.
 XX
 AC ADP46982;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Murine light chain variable anti-amphetamine antibody protein SeqID 38.
 XX
 KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
 KW PCP; drug addiction; antiaddictive; antibody therapy.
 XX
 OS Mus musculus.
 XX
 PN WO2004050032-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038384.
 PR 02-DEC-2002; 2002US-0430717P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
 PI Feng X;
 XX
 DR WPI; 2004-460981/43.
 XX
 PT New isolated antibody or its binding fragment that binds specifically to
 PT a drug of abuse, useful for treating a patient suffering from addiction
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 XX
 PS Claim 2; SEQ ID NO 38; 88pp; English.
 XX
 CC This invention relates to novel antibodies, or binding fragments thereof,
 CC that bind directly to various drugs of abuse. Specifically, it refers to
 CC human or chimeric monoclonal antibodies that are capable of binding to
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present
 CC invention describes generating hybridoma cell lines that produce such
 CC antibodies and transforming a cell with a gene encoding the antibody,
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can
 CC be used to treat a patient suffering from a drug addiction. Accordingly,
 CC these compositions exhibit antiaddictive activities and can be used for
 CC antibody therapy to treat patients suffering from a drug addiction. This
 CC polypeptide sequence is a murine light chain variable anti-amphetamine
 CC antibody of the invention.
 XX
 SQ Sequence 108 AA;

Query Match 90.5%; Score 503; DB 8; Length 108;
 Best Local Similarity 91.5%; Pred. No. 3.3e-28;
 Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106
 DB 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106

RESULT 11
 ADP46982
 ID ADP46982 standard; protein; 108 AA.
 XX
 AC ADP46982;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Murine light chain variable anti-amphetamine antibody protein SeqID 38.
 XX
 KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
 KW PCP; drug addiction; antiaddictive; antibody therapy.
 XX
 OS Mus musculus.
 XX
 PN WO2004050032-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038384.
 PR 02-DEC-2002; 2002US-0430717P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
 PI Feng X;
 XX
 DR WPI; 2004-460981/43.
 XX
 PT New isolated antibody or its binding fragment that binds specifically to
 PT a drug of abuse, useful for treating a patient suffering from addiction
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 XX
 PS Claim 2; SEQ ID NO 38; 88pp; English.
 XX
 CC This invention relates to novel antibodies, or binding fragments thereof,
 CC that bind directly to various drugs of abuse. Specifically, it refers to
 CC human or chimeric monoclonal antibodies that are capable of binding to
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present
 CC invention describes generating hybridoma cell lines that produce such
 CC antibodies and transforming a cell with a gene encoding the antibody,
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can
 CC be used to treat a patient suffering from a drug addiction. Accordingly,
 CC these compositions exhibit antiaddictive activities and can be used for
 CC antibody therapy to treat patients suffering from a drug addiction. This
 CC polypeptide sequence is a murine light chain variable anti-amphetamine
 CC antibody of the invention.
 XX
 SQ Sequence 108 AA;

Query Match 90.5%; Score 503; DB 8; Length 108;
 Best Local Similarity 91.5%; Pred. No. 3.3e-28;
 Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
 QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106
 DB 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPTKVDI 106


```

RESULT 12
AAU90905
ID AAU90905 standard; protein; 239 AA.
XX
AC AAU90905;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor-binding peptide #2861.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
XX ophthalmological; insulin; receptor; gene therapy; diabetes;
XX insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
XX diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US008528.
XX
PR 29-MAR-2000; 2000WO-US008528.
XX
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX
DR WPI; 2002-025774/03.
XX
PT Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
XX
PS Example 5; Fig 39; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention
XX
SQ Sequence 239 AA;
XX
Query Match 90.5%; Score 503; DB 5; Length 239;
Best Local Similarity 91.5%; Pred. No. 6.5e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQKPGKPKLLIYGASTLQSGVPS 60
DB 133 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPGKPKLLIYAASTLQSGVPS 192
QY 61 RFGSGSGGDTFTLTISLQPEDVATYYCOKFSSPPFTFGPTKVDI 106
DB 193 RFGSGSGGDTFTLTISLQPEDVATYYCOKYNSAPWTFQGKTKEI 238
XX
RESULT 13
AAU90904
ID AAU90904 standard; protein; 242 AA.

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XX
AC AAU90904;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor-binding peptide #2860.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
XX ophthalmological; insulin; receptor; gene therapy; diabetes;
XX insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
XX diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US008528.
XX
PR 29-MAR-2000; 2000WO-US008528.
XX
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX
DR WPI; 2002-025774/03.
XX
PT Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
XX
PS Example 5; Fig 38; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention
XX
SQ Sequence 242 AA;
XX
Query Match 90.3%; Score 502; DB 5; Length 242;
Best Local Similarity 90.6%; Pred. No. 7.8e-28;
Matches 96; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQKPGKPKLLIYGASTLQSGVPS 60
DB 136 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPGKPKLLIYAASTLQSGVPS 195
QY 61 RFGSGSGGDTFTLTISLQPEDVATYYCOKFSSPPFTFGPTKVDI 106
DB 196 RFGSGSGGDTFTLTISLQPEDVATYYCOKYNSAPWTFQGKTKEI 241
XX
RESULT 14
ADK18799
ID ADK18799 standard; protein; 107 AA.
XX
AC ADK18799;
XX

```

```
DT 06-MAY-2004 (first entry)
XX
XX DE Anti-human PDGF-D antibody protein related sequence #25.
XX
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO2003057857-A2.
XX
XX PD 17-JUL-2003.
XX
XX PF 06-JAN-2003; 2003WO-US000398.
XX
XX PR 07-JAN-2002; 2002US-00041860.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX DR WPI; 2003-587119/55.
XX
XX PT New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX PS Disclosure; SEQ ID NO 223; 255pp; English.
XX
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX SQ Sequence 107 AA;
XX
XX Query Match 90.1%; Score 501; DB 7; Length 107;
XX Best Local Similarity 91.5%; Pred. No. 4.5e-28;
XX Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYAASTLQSGVPS 60
QY 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKFSSPPFTFGPTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKYNSAPLTFGGGTKEI 106

RESULT 15
ADK18833
ID ADK18833 standard; protein; 107 AA.
XX
XX AC ADK18833;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Anti-human PDGF-D antibody protein related sequence #59.
XX
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO2003057857-A2.
XX
XX PD 17-JUL-2003.
XX
XX PF 06-MAY-2004 (first entry)
XX
XX PR 07-JAN-2002; 2002US-00041860.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX DR WPI; 2003-587119/55.
XX
XX PT New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX PS Disclosure; SEQ ID NO 223; 255pp; English.
XX
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX SQ Sequence 107 AA;
XX
XX Query Match 90.1%; Score 501; DB 7; Length 107;
XX Best Local Similarity 91.5%; Pred. No. 4.5e-28;
XX Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYAASTLQSGVPS 60
QY 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKFSSPPFTFGPTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKYNSAPLTFGGGTKEI 106
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PF 06-JAN-2003; 2003WO-US000398.
XX
XX PR 07-JAN-2002; 2002US-00041860.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX DR WPI; 2003-587119/55.
XX
XX PT New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX PS Disclosure; SEQ ID NO 257; 255pp; English.
XX
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX SQ Sequence 107 AA;
XX
XX Query Match 90.1%; Score 501; DB 7; Length 107;
XX Best Local Similarity 91.5%; Pred. No. 4.5e-28;
XX Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNYLAWYQOQPGKVPKLLIYAASTLQSGVPS 60
QY 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKFSSPPFTFGPTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKYNSAPLTFGGGTKEI 106

Search completed: November 16, 2005, 21:51:42
Job time : 62.3676 secs
```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-30
Perfect score: 556
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQKFSPPPTFGPGTKVDIS 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	87.9	131	2 S40352	Ig kappa chain V-J
2	479.5	86.2	107	2 S36275	Ig lambda chain V
3	470	84.5	132	2 S40334	Ig kappa chain - h
4	463	83.3	129	2 S52792	Ig kappa chain V r
5	462	83.1	107	2 S36269	Ig lambda chain V
6	460	82.7	95	2 PH0863	Ig kappa chain V r
7	460	82.7	107	2 S40366	Ig kappa chain V-J
8	459.5	82.6	124	2 S40336	Ig kappa chain V-J
9	459	82.6	108	2 B49047	Ig kappa chain V r
10	459	82.6	127	2 S40367	Ig kappa chain V-J
11	457	82.2	123	2 S40331	Ig kappa chain - h
12	455	81.8	107	2 S36264	Ig lambda chain V
13	455	81.8	125	2 S40349	Ig kappa chain V-J
14	454.5	81.7	108	2 S30521	Ig kappa chain V r
15	454	81.7	108	1 KIHUWE	Ig kappa chain V-I
16	453	81.5	125	2 S40333	Ig kappa chain V-J
17	452	81.3	117	2 S46376	Ig kappa chain V-J
18	451	81.1	108	2 S36279	Ig lambda chain V
19	451	81.1	127	2 S11240	Ig kappa chain V r
20	450	80.9	117	2 S46371	Ig kappa chain V-J
21	449	80.8	108	1 KIHUBN	Ig kappa chain V-I
22	449	80.8	110	2 S44118	Ig kappa chain V-J
23	448	80.6	107	2 S36262	Ig lambda chain V
24	448	80.6	108	2 S40330	Ig kappa chain V-J
25	448	80.6	108	2 S19674	Ig kappa chain V r
26	448	80.6	129	2 S40317	Ig kappa chain - h
27	447	80.4	108	1 KIHURE	Ig kappa chain V-I
28	447	80.4	129	2 S40369	Ig kappa chain - h
29	446	80.2	109	2 S31981	Ig kappa chain - h

RESULT 1

S40352
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40352
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40352
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLR>
A:Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 489; DB 2; Length 131;
Best Local Similarity 89.6%; Pred. No. 3e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGRVTITCRASQGRINYLAWYQQNPGKVPKLLIYGASTLQSGVPS	60
DB	21	DIQMTQSPSSLSASVGRVTITCRASQGSINVLAWYQQKPKVPKLLIYAASTLQSGVPS	80
QY	61	RFSGSGSGTDFTLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI	106
DB	81	RFSGSGSGTDFSLTITSSLPEDVATYYCQKNSVPRTFGQGTKEI	126

RESULT 2

S36275
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36275
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36275
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID:g939909
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 479.5; DB 2; Length 107;

Best Local Similarity 89.6%; Pred. No. 1.6e-34; Matches 95; Conservative 3; Mismatches 7; Indels 1; Gaps 1;	
QY	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 60
QY	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db	61 RFSGSGSGTDFLTITSSLOPEDVAVYYCQYISTP-TFGGQTKVEI 105
RESULT 3	
S40334	
Ig kappa chain - human	
C:Species: Homo sapiens (man)	
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000	
C:Accession: S40334	
R:Klein, R.; Jaenichen, R.; Zachau, H.G.	
Eur. J. Immunol. 23, 3248-3271, 1993	
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.	
A:Reference number: S40312; MUID:94080891; PMID:8258341	
A:Accession: S40334	
A:Status: preliminary; translation not shown	
A:Molecule type: mRNA	
A:Residues: 1-132 <KLE>	
A:Cross-references: EMBL:X72444	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:137-111/Domain: immunoglobulin homology <IMM>	
Query Match 84.5%; Score 470; DB 2; Length 132;	
Best Local Similarity 84.9%; Pred. No. 1.3e-33;	
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;	
QY	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db	22 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 81
QY	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db	82 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGGQTKVEI 127
RESULT 4	
S52792	
Ig kappa chain V region - human (fragment)	
C:Species: Homo sapiens (man)	
C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000	
C:Accession: S52792	
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,	
submitted to the EMBL Data Library, March 1995	
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-	
A:Reference number: S52789	
A:Accession: S52792	
A:Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-129 <ROC>	
A:Cross-references: EMBL:X85986; NID:g758598; PIDN:CAA59988.1; PID:g758599	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:138-112/Domain: immunoglobulin homology <IMM>	
Query Match 83.3%; Score 463; DB 2; Length 129;	
Best Local Similarity 84.9%; Pred. No. 5e-33;	
Matches 90; Conservative 3; Mismatches 13; Indels 0; Gaps 0;	
QY	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db	23 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 82
QY	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106

Db	83 RFSGSGSGADFTLTITSSLOPEDSATYYCQSYGTFTFGPGTKVDI 128
RESULT 5	
S36269	
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)	
C:Species: Homo sapiens (man)	
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000	
C:Accession: S36269	
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;	
EMBO J. 12, 725-734, 1993	
A:Title: Human anti-self antibodies with high specificity from phage display libraries.	
A:Reference number: S36256; MUID:93178448; PMID:7679990	
A:Accession: S36269	
A:Status: preliminary; nucleic acid sequence not shown	
A:Molecule type: mRNA	
A:Residues: 1-107 <GRI>	
A:Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:116-90/Domain: immunoglobulin homology <IMM>	
Query Match 83.1%; Score 462; DB 2; Length 107;	
Best Local Similarity 84.9%; Pred. No. 5.1e-33;	
Matches 90; Conservative 5; Mismatches 11; Indels 0; Gaps 0;	
QY	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db	1 DIQMTQSPSSLSASVGDRTVITTCRESQGIIRNDLGHYYQKPGKAPKLLIYGTSSLQSGVPS 60
QY	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db	61 RFSGSGSGTDFLTITSSLOPEDFATYYCQTTSPFLTFGGGTKLEI 106
RESULT 6	
PH0863	
Ig kappa chain V region (anti-DNA, III-2R) - human (fragment)	
C:Species: Homo sapiens (man)	
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004	
C:Accession: PH0863	
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.	
J. Exp. Med. 174, 1639-1652, 1991	
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.	
A:Reference number: PH0862; MUID:92078875; PMID:1660528	
A:Accession: PH0863	
A:Molecule type: DNA	
A:Residues: 1-95 <MAN>	
A:Cross-references: UNIPROT:Q9UL70	
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:1-23/Region: framework 1	
F:16-90/Domain: immunoglobulin homology <IMM>	
F:24-34/Region: complementarity-determining 1	
F:35-49/Region: framework 2	
F:50-56/Region: complementarity-determining 2	
F:57-88/Region: framework 3	
F:89-95/Region: complementarity-determining 3	
Query Match 82.7%; Score 460; DB 2; Length 95;	
Best Local Similarity 93.7%; Pred. No. 6.7e-33;	
Matches 89; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	
QY	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db	1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 60
QY	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPP 95
Db	61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKINSAP 95

```
RESULT 7
S40366
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40366
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40366
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-107 <KLE>
A:Cross-references: EMBL:X72476; NID:g441420; PIDN:CAAS1144.1; PID:g441421
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match      82.7%; Score 460; DB 2; Length 107;
Best Local Similarity 93.7%; Pred. No. 7.5e-33;
Matches 89; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 13 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYAASLQSGVPS 72
QY 61 RPSGSGSGTDFLTITSSLPQEDVATYYCQKPSPP 95
DB 73 RPSGSGSGTDFLTITSSLPQEDVATYYCQKYSAP 107

RESULT 8
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAAS1114.1; PID:g441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459.5; DB 2; Length 124;
Best Local Similarity 83.2%; Pred. No. 9.6e-33;
Matches 89; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 16 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYAASLQSGVPS 75
QY 61 RPSGSGSGTDFLTITSSLPQEDVATYYCQKPSPP 106
DB 76 RPSGSGSGTDFLTITSSLPQEDVATYYCQQLNTYPPWTFGQGTKEI 122

RESULT 9
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Viccor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
```

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A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes
A>Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 9.3e-33;
Matches 90; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYAASLQSGVPS 60
QY 61 RPSGSGSGTDFLTITSSLPQEDVATYYCQKPSPP 106
DB 61 RPSGSGSGTDFLTITSSLPQEDVATYYCQSYSTPLTFGGGTKEI 106

RESULT 10
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459; DB 2; Length 127;
Best Local Similarity 84.0%; Pred. No. 1.1e-32;
Matches 89; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 18 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQKPKAPKLLIYAASLQSGVPS 77
QY 61 RPSGSGSGTDFLTITSSLPQEDVATYYCQKPSPP 106
DB 78 RPSGSGSGTDFLTITSSLPQEDVATYYCQSYNTWTFGQGTKEI 123

RESULT 11
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:g441350; PIDN:CAAS1109.1; PID:g441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

Query Match	81.8%	Score 455;	DB 2;	Length 125;
Best Local Similarity	83.8%	Pred. No. 2.4e-32;		
Matches 88;	Conservative 8;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	2	IQMTQSSSLASVGDVRTIIICRASQGRINRYLAWYQQNPFQKVPKLLIYGASTLQSGVPSR	61	
Db	19	IOLTQTPSSLSASVGDVRTIIICRASQGISALAWYQKPFQKVPKLLIYGASTLQSGVPSR	78	

	Query Match	81.7%	Score 454;	DB 1;	Length 108;
	Best Local Similarity	82.1%;	Pred. No. 2.5e-32;		
	Matches	87;	Conservative	9;	Mismatches 10; Indels 0; Gaps 0;
Qy	1	DIQWTQSPSLASVGRVITTCRASGIRNYLAWYQONFGKVPKLLIYGASTLQSGVPS	60		
Db	1	DIQWTQSPSLASVGRVITTCRASGIRNDITWYQOKGTFAPKRLIYGASTLQSGVPS	60		
Qy	61	RFSGSGSGDTFTLTITSLQPEDVATYYCQKFSPPFTFGFGTKVDI	106		

Db 61 RFGSGSGTEFTLTINSLOPEDFATYYCLOYSSFPWTFGQGTKEV 106

Search completed: November 16, 2005, 22:04:09
Job time : 12.7849 secs

UNITED STATES DEPARTMENT OF AGRICULTURE
BUREAU OF PLANT INDUSTRY
WASHINGTON, D. C.

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-30
Perfect score: 556
Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CQKFSPPFTFGPGTKVDIS 107

Scoring table: BLOSUM62
Gapop'10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	498	89.6	108	2	Q9UL70	Q9UL70 homo sapien
2	480	86.3	236	2	Q6GMX8	Q6GMX8 homo sapien
3	458	82.4	236	2	Q6PIH7	Q6PIH7 homo sapien
4	454	81.7	108	1	KVIR_HUMAN	P01610 homo sapien
5	433	81.5	108	1	KVIY_HUMAN	P80362 homo sapien
6	450	80.9	236	2	Q7Z3Y4	Q7Z3Y4 homo sapien
7	449	80.8	108	1	KVIY_HUMAN	P04430 homo sapien
8	448	80.6	108	2	Q9UL77	Q9UL77 homo sapien
9	447	80.4	108	1	KVIO_HUMAN	P01607 homo sapien
10	445	80.0	236	2	Q6GMW1	Q6GMW1 homo sapien
11	443.5	79.8	107	2	Q9UL81	Q9UL81 homo sapien
12	442.5	79.6	107	2	Q96SA9	Q96SA9 homo sapien
13	442	79.5	244	2	Q65ZC8	Q65ZC8 homo sapien
14	440	79.1	129	1	KVIV_HUMAN	P04431 homo sapien
15	439	79.0	108	1	KVIP_HUMAN	P01608 homo sapien
16	439	79.0	108	1	KVIQ_HUMAN	P01609 homo sapien
17	437	78.6	108	1	KVIM_HUMAN	P01605 homo sapien
18	437	78.6	240	2	Q65ZC9	Q65ZC9 homo sapien
19	436.5	78.5	107	1	KVID_HUMAN	P01596 homo sapien
20	436	78.4	236	2	Q6GMX0	Q6GMX0 homo sapien
21	435	78.2	108	1	KVIE_HUMAN	P01597 homo sapien
22	434	78.1	108	1	KVIB_HUMAN	P01594 homo sapien
23	434	78.1	108	1	KVIG_HUMAN	P01599 homo sapien
24	434	78.1	108	1	KVIH_HUMAN	P01611 homo sapien
25	432	77.7	108	1	KVIS_HUMAN	Q9UL79 homo sapien
26	431	77.5	236	2	Q6GMX9	Q6GMX9 homo sapien
27	431	77.5	236	2	Q6PIT5	Q6PIT5 homo sapien
28	431	77.5	236	2	Q6PIT5	Q6PIT5 homo sapien
29	430	77.3	108	1	KVIL_HUMAN	P01598 homo sapien
30	427	76.8	108	1	KVIF_HUMAN	P01598 homo sapien
31	425	76.4	234	2	Q7Z473	Q7Z473 homo sapien

32	424	76.3	108	1	KVIA_HUMAN	P01593 homo sapien
33	419	75.4	129	1	KVIX_HUMAN	P04432 homo sapien
34	418	75.2	108	1	KVIK_HUMAN	P01603 homo sapien
35	417	75.0	236	2	Q6PIH4	Q6PIH4 homo sapien
36	414	74.5	108	1	KVIC_HUMAN	P01595 homo sapien
37	414	74.5	108	1	KVIN_HUMAN	P01606 homo sapien
38	413	74.3	116	2	Q96PF6	Q96PF6 homo sapien
39	412	74.1	117	1	KVII_HUMAN	P01601 homo sapien
40	410.5	73.8	109	1	KVIJ_HUMAN	P01612 homo sapien
41	407	73.2	117	1	KVIJ_HUMAN	P01602 homo sapien
42	399	71.8	109	2	Q920E6	Q920E6 mus musculu
43	397	71.4	134	1	KV4C_HUMAN	P06314 homo sapien
44	396	71.2	114	1	KV4A_HUMAN	P01625 homo sapien
45	392	70.5	298	2	Q9QYF0	Q9QYF0 synthetic c

ALIGNMENTS

RESULT 1
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 89.6%; Score 498; DB 2; Length 108;
Best Local Similarity 90.6%; Pred. No. 2.8e-43;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQKVPKLLIYGASTLQSGVPS	60
Db	1	DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQKPKGKPKSLIYAAASTLQSGVPS	60
QY	61	RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI	106
Db	61	RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKLEI	106

RESULT 2
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 RT in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 CC -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 CC against 3,4-pyruvylated galactose and isolated from a patient with
 CC Waldenström's macroglobulinemia.

CC PIR; A01876; K1HUWE.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KW Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61P0945618C CRC64;

Query Match 81.7%; Score 454; DB 1; Length 108;
 Best Local Similarity 82.1%; Pred. No. 9e-39;
 Matches 87; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQNPQKPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNLDITWYQKPGTAPKRLIYGASTLQSGVPS 60
 QY 61 RFGSGSGGDTFTLTISLQPEDVATYVYCKFSSPPPTFGTGVKDI 106
 DB 61 RFGSGSGGDTFTLTISLQPEDVATYVYCLQSSFPWTFQGTGVKVEV 106

RESULT 5
 KVIY_HUMAN STANDARD; PRT; 108 AA.
 ID KVIY_HUMAN
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RL Biochemistry 33:14848-14857 (1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VI-
 RT related fragment of the human kappa Bence Jones protein wat.";
 RL J. Mol. Biol. 147:185-193 (1981).

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB; 1WTL; X-ray; A/B=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT TURN 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;

Query Match 81.5%; Score 453; DB 1; Length 108;
 Best Local Similarity 80.2%; Pred. No. 1.1e-38;
 Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQNPQKPKLLIYGASTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDITVYNNWFOQRPQAPKRLIYGASILETGVP 60
 QY 61 RFGSGSGGDTFTLTISLQPEDVATYVYCKFSSPPPTFGTGVKDI 106
 DB 61 RFGSGSGGDTFTLTISLQPEDVATYVYCOQYDTLPLTFGGTGVKDI 106

RESULT 6
 Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
 ID Q7Z3Y4
 AC Q7Z3Y4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

61 RPSGSGTDTFTLTSSLPQDPATYYCQSYSTSWTFGEQTKVEI 106

Db

RESULT 9

KVIO HUMAN

ID KVIO HUMAN STANDARD; PRT; 108 AA.

AC F01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig kappa chain V-I region Rei.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE.

RX MEDLINE=7603758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rei refined at 2.0-A resolution.";

RL Biochemistry 14:4943-4952 (1975).

CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A91663; KIHURE.

DR PDB; 1AR2; X-ray; @=1-107.

DR PDB; 1BWV; X-ray; A/B=1-107.

DR PDB; 1REI; X-ray; A/B=1-107.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

KW 3D-structure; Bence-Jones protein; Direct protein sequencing;

FT DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 8

FT STRAND 4 7

FT STRAND 10 13

FT STRAND 15 16

FT STRAND 19 25

FT STRAND 30 31

FT STRAND 33 38

FT STRAND 40 41

FT STRAND 45 49

FT STRAND 50 52

FT STRAND 53 54

FT STRAND 56 57

FT STRAND 60 61

FT STRAND 62 67

FT STRAND 69 69

FT STRAND 70 75

FT HELIX 80 82

FT STRAND 84 90

FT STRAND 97 98

FT STRAND 102 106

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 80.4%; Score 447; DB 1; Length 108;

Best Local Similarity 79.4%; Pred. No. 4.7e-38;

Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVDRVITTCRASQIGIRNVLANYQNPQGVKPLLIYTGASTLQSGVPS 60

DB 1 DIQMTQSPSSLSASVGVDRVITTCRASQIGIRNVLANYQNPQGVKPLLIYTGASTLQSGVPS 60

QY 61 RPSGSGTDTFTLTSSLPQDPATYYCQSYSTSWTFGEQTKVDIS 107

DB 61 RPSGSGTDTFTLTSSLPQDPATYYCQSYSTSWTFGEQTKVDIS 107

RESULT 10

Q6GMW1

ID Q6GMW1 PRELIMINARY; PRT; 236 AA.

AC Q6GMW1; (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE-Spleen;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE-Spleen;

RA Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073791; AAH73791.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.


```
QY 1 DIQMTQSPSSLSASVCDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 137 DIQMTQSPSTLSASTGDRVTITTCRASEGIYHNLAWYQKPGKAPFLIYKASSLASGAPS 196
QY 61 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVDI 106
Db 197 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKLEI 242

RESULT 14
KV1W HUMAN STANDARD; PRT; 129 AA.
AC P0431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Framework-3.
FT DOMAIN 79 110 Complementarity-determining-2.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; P941FA07D4AFC9F9 CRC64;

Query Match 79.1%; Score 440; DB 1; Length 129;
Best Local Similarity 82.1%; Pred. No. 3e-37;
Matches 87; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVCDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 23 DIQMTQSPSSLSASVCDRTVITTCRASQISNYLAWYQKPGKAPKLLIYAASLQSGVTS 82
QY 61 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVDI 106
Db 83 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKLEI 128
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RESULT 15

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ID KV1P HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL York (1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A91638; KIHURY.
CC HSSP; P01607; 1BMW.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; FSACEDE5A313DF3A CRC64;

Query Match 79.0%; Score 439; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 3.1e-37;
Matches 84; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVCDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVCDRTVITTCRASQDISFLNYQKPGKAPKLLIYDASKLEAGVPS 60
QY 61 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVD 105
Db 61 RFSGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVD 105
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Search completed: November 16, 2005, 22:01:54
Job time : 60.9908 secs

THE BIBLE IN THE MIDDLE

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-30
Perfect score: 556
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....CQKFSPPFTFGPGTKVDIS 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aaa/5B_COMB.pep:*
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4: /cgn2_6/prodata/1/aaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/aaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	90.1	107	3	US-08-599-226-9
2	501	90.1	107	3	US-09-125-098-9
3	501	90.1	107	4	US-09-540-018-9
4	499	89.7	107	3	US-08-599-226-1
5	499	89.7	107	3	US-09-125-098-1
6	499	89.7	107	4	US-09-540-018-1
7	483	86.9	107	1	US-08-276-852-84
8	483	86.9	107	1	US-08-899-575-84
9	483	86.9	107	5	PCT-US95-08743-84
10	483	86.9	107	5	PCT-US95-08743-84
11	480	86.3	214	4	US-09-472-087-71
12	475	85.4	106	1	US-08-276-852-83
13	475	85.4	106	1	US-08-899-575-83
14	475	85.4	106	1	US-08-899-575-83
15	475	85.4	106	5	PCT-US95-08743-83
16	475	85.4	107	1	US-08-276-852-82
17	475	85.4	107	1	US-08-899-575-82
18	475	85.4	107	1	US-08-899-575-82
19	475	85.4	107	2	US-07-934-373C-18
20	475	85.4	107	3	US-08-437-642B-18
21	475	85.4	107	4	US-08-146-206C-18
22	475	85.4	107	4	US-09-648-067A-14
23	475	85.4	107	4	US-09-705-686-18
24	475	85.4	107	4	US-09-705-392A-18
25	475	85.4	107	4	US-09-705-398-18
26	475	85.4	107	5	PCT-US93-07832-18
27	475	85.4	107	5	PCT-US95-08743-82

28	475	85.4	108	3	US-08-974-899-3	Sequence 3, Appli
29	475	85.4	108	4	US-09-795-798-3	Sequence 3, Appli
30	473.5	85.2	108	3	US-09-240-274-177	Sequence 177, App
31	470	84.5	109	2	US-07-934-373C-3	Sequence 3, Appli
32	470	84.5	109	3	US-08-437-642B-3	Sequence 3, Appli
33	470	84.5	109	4	US-08-146-206C-3	Sequence 3, Appli
34	470	84.5	109	4	US-09-705-686-3	Sequence 3, Appli
35	470	84.5	109	4	US-09-705-392A-3	Sequence 3, Appli
36	470	84.5	109	4	US-09-705-398-3	Sequence 3, Appli
37	470	84.5	109	5	PCT-US93-07832-3	Sequence 3, Appli
38	469	84.4	106	1	US-08-276-852-85	Sequence 85, Appl
39	469	84.4	106	1	US-08-899-575-85	Sequence 85, Appl
40	469	84.4	106	1	US-08-899-575-85	Sequence 85, Appl
41	469	84.4	106	5	PCT-US95-08743-85	Sequence 85, Appl
42	469	84.4	108	3	US-09-025-769B-14	Sequence 14, Appl
43	469	84.4	108	4	US-09-490-070A-14	Sequence 14, Appl
44	469	84.4	108	4	US-09-490-153-14	Sequence 14, Appl
45	469	84.4	108	4	US-09-490-324-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-599-226-9
; Sequence 9, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

US-08-599-226-9

Query Match 90.1%; Score 501; DB 3; Length 107;
Best Local Similarity 89.6%; Pred. No. 5.9e-37;
Matches 95; Conservative 5; Mismatches 6; Indels

Qy 1 DIQMTQSPSSLSASGDRVTITCRASQIRNYLAWYQQNPGKVPKLLIYGASTIQSGVPS 60
|||||:|||||

Db 1 DIQMTQSPSSLSASIGDRVTITCRASQIRNYLAWYQQNPGKAPKLLIYAASTIQSGVPS 60
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QY 61 RFGSGSGTDFTLTISIQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 |||||
 Db 61 RFGSGSGTDFTLTISIQPEDVATYYCQKYNAPYAFGGQTKVEI 106
 |||||

RESULT 2
US-09-125-098-9
; Sequence 9, Application US/09125098
; Patent No. 6258562
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts

Query Match 90.1%; Score 501; DB 3; Length 107;
Best Local Similarity 89.6%; Pred. No. 5.9e-37;
Matches 95. Conservative 5. Mismatches 6. Indels

[illegible]

RESULT 3
US-09-540-018-9
Sequence 9, Application US/09540018
Patent No. 6509015
GENERAL INFORMATION:
APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakcalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNF α
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018
FILING DATE: 31-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-540-018-9

Query Match	90.1%	Score 501;	DB 4;	Length 107;
Best Local Similarity	89.6%	Pred. No. 5..9e-37;		
Matches	95;	Mismatches 5;	Indels 6;	Gaps 0;
	Conservative			

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pB	1	DIQWTQSPSSISASIGDRVTITCRASQIRNYLAWYQONPGKAPKLLIYAASTLQSGVPS	60

QY 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKNSAPYAFGQGTKVEI 106

RESULT 4

US-08-599-226-1
; Sequence 1, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-599-226-1

Query Match 89.7%; Score 499; DB 3; Length 107;
Best Local Similarity 89.6%; Pred. No. 8.8e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPQKVPKLLIYAASSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 RFGSGSGTDFLTITSSLOPEDVATYYCQRYNRPAPYTFGQGTKVEI 106

RESULT 5

US-09-125-098-1
; Sequence 1, Application US/09125098

; Patent No. 6258562
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-125-098-1

Query Match 89.7%; Score 499; DB 3; Length 107;
Best Local Similarity 89.6%; Pred. No. 8.8e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPQKVPKLLIYAASSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 RFGSGSGTDFLTITSSLOPEDVATYYCQRYNRPAPYTFGQGTKVEI 106

RESULT 6

US-09-540-018-1
; Sequence 1, Application US/09540018
; Patent No. 6509015
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.

```
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/540,018
; FILING DATE: 31-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-540-018-1

Query Match 89.7%; Score 499; DB 4; Length 107;
Best Local Similarity 89.6%; Pred. No. 8.8e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DQMTQSPSSLSASVGDRTVITCRASQGINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DQMTQSPSSLSASVGDRTVITCRASQGINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
QY 61 RSGSGSGDTFTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106
Db 61 RSGSGSGDTFTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106

RESULT 7
US-08-276-852-84
; Sequence 84, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
```

```
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-84

Query Match 86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGINYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGDRTVITCRASQGINYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 60
QY 63 SGGSGGTDTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106
Db 61 SGGSGGTDTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106

RESULT 8
US-08-899-575-84
; Sequence 84, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US 08/899,575
/ APPLICATION DATA:
/ FILING DATE: 24-JUL-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCRI452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-899-575-84

Query Match      86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSIQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSIQPEDVATYYCQKNSAPRTFGQGTKEI 104

RESULT 9
US-08-899-575-84
/ Sequence 84, Application US/08899575
/ Patent No. 5804440
/ GENERAL INFORMATION:
/ APPLICANT: Burton, Dennis R
/ APPLICANT: Barbas, Carlos F
/ APPLICANT: Lerner, Richard A
/ TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
/ NUMBER OF SEQUENCES: 170
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: The Scripps Research Institute, Office of
/ ADDRESSEE: Patent Counsel
/ STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
/ STREET: Mail Drop TPC8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/899,575
/ FILING DATE: 24-JUL-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
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/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCRI452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-899-575-84

Query Match      86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSIQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSIQPEDVATYYCQKNSAPRTFGQGTKEI 104

RESULT 10
PCT-US95-08743-84
/ Sequence 84, Application PC/TUS9508743
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
/ NUMBER OF SEQUENCES: 170
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/08743
/ FILING DATE: 11-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-08743-84

Query Match      86.9%; Score 483; DB 5; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSIQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSIQPEDVATYYCQKNSAPRTFGQGTKEI 104
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RESULT 11
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-71

Query Match      86.3%; Score 480; DB 4; Length 214;
Best Local Similarity 86.8%; Pred. No. 8.1e-35;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTVITCRASQSIINSYLDWYQOKPKAPKLLIYAASSLQSGVPS 60

Qy 61 RFSGSGGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDI 106
Db 61 RFSGSGGTDFTLTISSLPQEDFATYYCQYYSTPTFTFGPGTKVEI 106

RESULT 12
US-08-276-852-83
; Sequence 83, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

RESULT 13
US-08-899-575-83
; Sequence 83, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

; Query Match      85.4%; Score 475; DB 1; Length 106;
; Best Local Similarity 86.5%; Pred. No. 1.1e-34;
; Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGIIRNYLAWYQORPGKVPRLIYAASTLQSGVPTRF 60

Qy 63 SGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDI 106
Db 61 SGSGSGTDFTLTISSLPQEDVATYYCQKINSVPTFTFGGTKEI 104
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; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-83

Query Match      85.4%; Score 475; DB 1; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPKGVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGTKVEI 104

RESULT 14
US-08-899-575-83
; Sequence 83, Application US/08899575
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-83

Query Match      85.4%; Score 475; DB 1; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPKGVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGTKVEI 104

RESULT 15
PCT-US95-08743-83
; Sequence 83, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-83

Query Match      85.4%; Score 475; DB 5; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPKGVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGTKVEI 104

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds
(without alignments)
681.481 Million cell updates/sec

Title: US-10-660-357A-30
Perfect score: 556
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....CQKFSPPPTFGGTRKVDIS 107

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
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17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep.*
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19: /cgn2_6/prodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	556	100.0	107	14	US-10-330-530-30
3	556	100.0	107	16	US-10-660-357-30
4	520	93.5	107	17	US-10-727-155-306
5	520	93.5	108	17	US-10-725-962-40
6	508	91.4	107	17	US-10-727-155-264
7	505	90.8	107	15	US-10-041-860-346
8	503	90.5	107	15	US-10-309-762-86
9	503	90.5	108	17	US-10-725-962-36
10	503	90.5	108	17	US-10-725-962-38
11	501	90.1	107	10	US-09-801-185A-9
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Sequence 30, Appl					
Sequence 30, Appl					
Sequence 306, Appl					
Sequence 40, Appl					
Sequence 264, Appl					
Sequence 346, Appl					
Sequence 86, Appl					
Sequence 36, Appl					
Sequence 38, Appl					

12	501	90.1	107	14	US-10-041-860-32	Sequence 32, Appl
13	501	90.1	107	14	US-10-041-860-223	Sequence 223, App
14	501	90.1	107	14	US-10-041-860-257	Sequence 257, App
15	501	90.1	107	15	US-10-133-715-9	Sequence 9, Appl
16	501	90.1	107	15	US-10-302-356A-9	Sequence 9, Appl
17	501	90.1	107	15	US-10-163-657A-9	Sequence 9, Appl
18	501	90.1	107	15	US-10-422-287-9	Sequence 9, Appl
19	501	90.1	107	16	US-10-622-932-9	Sequence 9, Appl
20	501	90.1	107	16	US-10-623-065-9	Sequence 9, Appl
21	501	90.1	107	16	US-10-623-076-9	Sequence 9, Appl
22	501	90.1	107	16	US-10-622-210-9	Sequence 9, Appl
23	501	90.1	107	16	US-10-623-035-9	Sequence 9, Appl
24	501	90.1	107	16	US-10-623-075-9	Sequence 9, Appl
25	501	90.1	107	16	US-10-665-383-44	Sequence 44, Appl
26	501	90.1	107	16	US-10-622-928-9	Sequence 9, Appl
27	501	90.1	107	16	US-10-622-205-9	Sequence 82, Appl
28	501	90.1	244	10	US-09-880-748-82	Sequence 164, App
29	501	90.1	244	10	US-09-880-748-164	Sequence 261, App
30	501	90.1	244	10	US-09-880-748-261	Sequence 82, Appl
31	501	90.1	244	15	US-10-293-418-82	Sequence 164, App
32	501	90.1	244	15	US-10-293-418-164	Sequence 261, App
33	501	90.1	244	15	US-10-293-418-261	Sequence 41, Appl
34	500	89.9	108	17	US-10-725-962-41	Sequence 1, Appl
35	499	89.7	107	10	US-09-801-185A-1	Sequence 39, Appl
36	499	89.7	107	14	US-10-041-860-39	Sequence 222, App
37	499	89.7	107	14	US-10-041-860-222	Sequence 256, App
38	499	89.7	107	15	US-10-133-715-1	Sequence 1, Appl
39	499	89.7	107	15	US-10-302-356A-1	Sequence 1, Appl
40	499	89.7	107	15	US-10-163-657A-1	Sequence 1, Appl
41	499	89.7	107	15	US-10-422-287-1	Sequence 1, Appl
42	499	89.7	107	16	US-10-622-932-1	Sequence 1, Appl
43	499	89.7	107	16	US-10-623-065-1	Sequence 1, Appl
44	499	89.7	107	16	US-10-623-076-1	Sequence 1, Appl
45	499	89.7	107	16	US-10-623-075-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-330-613-30
; Sequence 30, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-30

Query Match 100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGDRVTITCRASQGRNRYLAWYQNPQPKVKLLIYGASTLQSGVPS	60
Db	1	DIQMTQSPSSLSASVGDRVTITCRASQGRNRYLAWYQNPQPKVKLLIYGASTLQSGVPS	60
Qy	61	RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPPTFGGTRKVDIS	107
Db	61	RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPPTFGGTRKVDIS	107

RESULT 2

```
US-10-330-530-30
; Sequence 30, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-30

Query Match          100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107
Db      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 3
US-10-660-357-30
; Sequence 30, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-30

Query Match          100.0%; Score 556; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107
Db      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 4
US-10-727-155-306
; Sequence 306, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchro
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-306

Query Match          93.5%; Score 520; DB 17; Length 107;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDI 106
Db      61 RFGSGSGTDFTLTISLQPEDVATYYCQKFSPPPTFGPTKVDI 106

RESULT 5
US-10-725-962-40
; Sequence 40, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071A
; CURRENT APPLICATION NUMBER: US/10/725,962
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-40

Query Match          93.5%; Score 520; DB 17; Length 108;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
; APPLICANT: John S. Babcock
```

```

Db      1 DIQWTPSPSLASVGDVRTITCRASQGISNYLAWYQKPGVKPKLLIYAASTLQSGVPS 60
Qy      61 RFSGSGGTDFTLTITSSLPQEDVATYYCQKFSPPPTFGFGTKVDI 106
        |||
Db      61 RFSGSGGTDFTLTITSSLPQEDVATYYCQKFSPPPTFGFGTKVDI 106
        |||

RESULT 6
US-10-727-155-264
; Sequence 264, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaespal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaeella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: AGENIX.073A
; CURRENT APPLICATION NUMBER: US/10727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-264

Query Match          91.4%; Score 508; DB 17; Length 107;
Best Local Similarity 91.5%; Pred. No. 3.9e-35;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0

Qy      1 DIQWTPSPSLASVGDVRTITCRASQGISNYLAWYQKPGVKPKLLIYAASTLQSGVPS 60
Db      1 DIQWTPSPSLASVGDVRTITCRASQGISNYLAWYQKPGVKPKLLIYAASTLQSGVPS 60
Qy      61 RFSGSGGTDFTLTITSSLPQEDVATYYCQKFSPPPTFGFGTKVDI 106
        |||
Db      61 RFSGSGGTDFTLTITSSLPQEDVATYYCQKFSPPPTFGFGTKVDI 106
        |||

RESULT 7
US-10-041-860-346
; Sequence 346, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07

```

```
; PRIOR APPLICATION NUMBER: 60/430717
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-36

Query Match          90.5%; Score 503; DB 17; Length 108;
Best Local Similarity 91.5%; Pred. No. 1e-34;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLTQSGVPS 60
   |||||

QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
   |||||
DB 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVEI 106
   |||||

RESULT 10
US-10-725-962-38
; Sequence 38, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071A
; CURRENT APPLICATION NUMBER: US/10/725,962
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-38

Query Match          90.5%; Score 503; DB 17; Length 108;
Best Local Similarity 91.5%; Pred. No. 1e-34;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLTQSGVPS 60
   |||||

QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
   |||||
DB 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVEI 106
   |||||

RESULT 11
US-09-801-185A-9
; Sequence 9, Application US/09801185A
; Publication No. US20030092059A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
```

```
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/801,185A
; FILING DATE: 07-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,226
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 60/031,476
; FILING DATE: 25-NOV-1996
; APPLICATION NUMBER: US 09/125,098
; FILING DATE: 07-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-801-185A-9

Query Match          90.1%; Score 501; DB 10; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.5e-34;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLTQSGVPS 60
   |||||

QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
   |||||
DB 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPFTFGPGTKVEI 106
   |||||

RESULT 12
US-10-041-860-32
; Sequence 32, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
```

```
US-10-041-860-32
Query Match      90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLQSGVPS 60
QY 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106
DB 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVEI 106

RESULT 13
US-10-041-860-223
; Sequence 223, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-223

Query Match      90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLQSGVPS 60
QY 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106
DB 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVEI 106

RESULT 14
US-10-041-860-257
; Sequence 257, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-257

Query Match      90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGRKPKLLIYAASLQSGVPS 60
QY 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106
DB 61 RFGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVEI 106

Search completed: November 16, 2005, 23:05:44
Job time : 65.6949 secs
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THE END OF THE LINE (1970)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-34
Perfect score: 556
Sequence: 1 ELVMTQSPATLSVSPGERAT.....COQYNWPTFGQTKYVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	7	Adc99805 Anti-huma
2	556	100.0	107	7	Add05409 Anti-MUC1
3	556	100.0	107	7	Add05442 Anti-MUC1
4	556	100.0	107	7	Adf09847 Human ant
5	546	98.2	107	7	Adc99777 Anti-huma
6	546	98.2	107	7	Add05381 Anti-MUC1
7	546	98.2	107	7	Adf09819 Human ant
8	534	96.0	107	6	Abr54896 Light cha
9	530	95.3	107	6	Abr54900 Light cha
10	527	94.8	107	6	Abr54897 Light cha
11	527	94.8	107	6	Abr54883 Light cha
12	527	94.8	107	8	Adp22404 Human ant
13	527	94.8	107	8	Adp22407 Human ant
14	527	94.8	107	8	Adr31547 L16/JK4 h
15	527	94.8	107	8	Abr54891 Light cha
16	525	94.4	107	6	Abr54906 Light cha
17	524.5	94.3	108	6	Abr54893 Light cha
18	524	94.2	107	6	Abr54893 Light cha
19	524	94.2	107	8	Adp22408 Human ant
20	523	94.1	250	5	Abp45941 Human Bly
21	523	94.1	250	7	Adg96768 Single ch
22	521	93.7	107	6	Abr54889 Light cha
23	520.5	93.6	117	3	Aay99557 Human LHL
24	520.5	93.6	117	6	Abw02456 Tumour-sp
25	520.5	93.6	117	6	Abw02458 Tumour-sp

26	520.5	93.6	117	6	Abw02456 Tumour-sp
27	520.5	93.6	117	6	Abw02456 Tumour-sp
28	520.5	93.6	117	7	Abw02446 Human mon
29	520.5	93.6	117	7	Abw02466 Human mon
30	520.5	93.6	117	7	Abw02466 Human mon
31	520	93.5	246	5	Abp45257 Human Bly
32	520	93.5	246	7	Adg96084 Single ch
33	517	93.0	107	7	Adh080364 Human ant
34	516	92.8	107	8	Adp22278 Human ant
35	516	92.8	107	8	Adp22278 Human ant
36	516	92.8	127	7	Adc61110 Human ant
37	515.5	92.7	106	8	Adp22371 Human ant
38	515	92.6	154	8	Adl25472 Human mAb
39	513.5	92.4	117	6	Abw02456 Tumour-sp
40	513.5	92.4	117	6	Abw02456 Tumour-sp
41	513.5	92.4	117	6	Abw02456 Tumour-sp
42	513.5	92.4	117	6	Abw02456 Tumour-sp
43	513.5	92.4	117	7	Abw02460 Human mon
44	513.5	92.4	117	7	Abw02462 Human mon
45	513.5	92.4	117	7	Abw02459 Human mon

ALIGNMENTS

RESULT 1
Adc99805
ID ADC99805 standard; protein; 107 AA.
XX
AC ADC99805;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99807.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 3; SEQ ID NO 34; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 556; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RFGSGSGTEFTLTISLQSEDFAVYCCQYNNWPRFTGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQSEDFAVYCCQYNNWPRFTGGTKVEIK 107

RESULT 2

ADD05409

ID ADD05409 standard; protein; 107 AA.

XX

AC ADD05409;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 34.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX

KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX

OS Homo sapiens.

XX

PN WO2003057006-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

XX

PI Gudas J, Bar-Eli M;

XX

DR WPI; 2003-577496/54.

XX

DR N-PSDB; ADD05411.

XX

PS Claim 3; SEQ ID NO 34; 87pp; English.

XX

XX The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody light chain, variable region,

CC protein of the invention.

XX

SQ Sequence 107 AA;

XX

Query Match 100.0%; Score 556; DB 7; Length 107;

Db

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RFGSGSGTEFTLTISLQSEDFAVYCCQYNNWPRFTGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQSEDFAVYCCQYNNWPRFTGGTKVEIK 107

RESULT 3

ADD05442

ID ADD05442 standard; protein; 107 AA.

XX

AC ADD05442;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID 67.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX

KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX

OS Unidentified.

XX

PN WO2003057006-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

XX (ABGE-) ABGENIX INC.

XX

PI Gudas J, Bar-Eli M;

XX

DR WPI; 2003-577496/54.

XX

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX

PS Disclosure; SEQ ID NO 67; 87pp; English.

XX

XX The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody light chain, variable region,

CC protein of the invention.

XX

SQ Sequence 107 AA;

XX

Query Match 100.0%; Score 556; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107
 DB 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107

RESULT 4
 ADF09847
 ID ADF09847 standard; protein; 107 AA.
 AC ADF09847;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human anti-MUC18 monoclonal antibody light chain #9.
 KW cell proliferation inhibition; MUC18 tumour antigen;
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 KW carcinoma; cancer; malignancy; light chain; human.
 XX
 OS Homo sapiens.
 PN WO2003057837-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041580.
 XX
 PR 28-DEC-2001; 2001US-0346414P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J;
 XX
 DR WPI: 2003-598367/56.
 DR N-PSDB; ADF09849.
 XX
 XX Inhibiting cell proliferation associated with expression of MUC18 tumour
 PT antigen, involves incubating and inhibiting cell by administering anti-
 PT MUC18 monoclonal antibody.
 XX
 PS Claim 3; SEQ ID NO 34; 83pp; English.
 XX
 CC The invention comprises a method for inhibiting cell proliferation
 CC associated with expression of MUC18 tumour antigen. The method involves
 CC administering anti-MUC18 monoclonal antibody. The method of the invention
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
 CC proliferation associated with the expression of MUC18 tumour antigen, the
 CC method is preferably useful for inhibiting tumour metastasis. The method
 CC is useful for inhibiting cell proliferation in patients with tumours,
 CC carcinomas, cancer and other malignancies. The present amino acid
 CC sequence represents a light chain from an MUC18 tumour antigen-specific
 CC monoclonal antibody.
 XX
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 556; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.1e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLLIFGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107
 DB 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107

RESULT 5
 ADC99777
 ID ADC99777 standard; protein; 107 AA.
 XX

AC ADC99777;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6.
 XX
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057838-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041581.
 XX
 PR 28-DEC-2001; 2001US-0346299P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J;
 XX
 DR WPI: 2003-587113/55.
 DR N-PSDB; ADC9779.
 XX
 XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.
 XX
 PS Claim 3; SEQ ID NO 6; 78pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC light chain protein of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 98.2%; Score 546; DB 7; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.7e-33;
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLLIFGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107
 DB 61 RPSGSGTGTEFTLTISLQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107

RESULT 6
 ADD05381
 ID ADD05381 standard; protein; 107 AA.
 XX
 AC ADD05381;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 6.
 XX
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.

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XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041582.
XX PR 28-DEC-2001; 2001US-0346460P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX WPI; 2003-577496/54.
XX N-PSDB; ADD05383.
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX associated with melanoma, or increasing survival of an animal having a
XX metastatic tumor.
XX Claim 3; SEQ ID NO 6; 87pp; English.
XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumor growth in an animal. The tumor inhibition process comprises
XX selecting an animal in need of treatment for a tumor, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumor with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or
XX tumor metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumor. This
XX sequence represents an anti-MUC18 antibody light chain, variable region,
XX of the invention.
XX Sequence 107 AA;
Query Match 98.2%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVWTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
DB 1 EIVWTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITSSLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
RESULT 7
ADF09819
ID ADF09819 standard; protein; 107 AA.
XX AC ADF09819;
XX DT 12-FEB-2004 (first entry)
XX DE Human anti-MUC18 monoclonal antibody light chain #2.
XX cell proliferation inhibition; MUC18 tumour antigen;
XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
XX carcinoma; cancer; malignancy; light chain; human.
XX OS Homo sapiens.
XX PN WO2003057837-A2.

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XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041580.
XX PR 28-DEC-2001; 2001US-0346414P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX WPI; 2003-598367/56.
XX N-PSDB; ADF09821.
XX Inhibiting cell proliferation associated with expression of MUC18 tumor
XX antigen, involves incubating and inhibiting cell by administering anti-
XX MUC18 monoclonal antibody.
XX Claim 3; SEQ ID NO 6; 83pp; English.
XX The invention comprises a method for inhibiting cell proliferation
XX associated with expression of MUC18 tumour antigen. The method involves
XX administering anti-MUC18 monoclonal antibody. The method of the invention
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX proliferation associated with the expression of MUC18 tumour antigen, the
XX method is preferably useful for inhibiting tumour metastasis. The method
XX is useful for inhibiting cell proliferation in patients with tumours,
XX carcinomas, cancer and other malignancies. The present amino acid
XX sequence represents a light chain from an MUC18 tumour antigen-specific
XX monoclonal antibody.
XX Sequence 107 AA;
Query Match 98.2%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVWTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
DB 1 EIVWTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITSSLSQSEDFAVYYCQYNNWPRFTFGGQTKVEIK 107
RESULT 8
ABR54896
ID ABR54896 standard; protein; 107 AA.
XX AC ABR54896;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3A9 SEQ ID NO:122.
XX Engineered template; single primer amplification; antibody library;
XX nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX 19-SEP-2002; 2002WO-US029889.
XX 19-SEP-2001; 2001US-0323455P.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;

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XX PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
 XX DR WPI; 2003-313359/30.
 XX
 PT Amplifying nucleic acid by contacting engineered nucleic acid strand
 PT having predetermined sequence at one end and sequence complementary to
 PT predetermined sequence at other end, with primer having predetermined
 PT sequence.
 XX
 PS Example 3; Fig 8b-c; 68pp; English.
 XX
 CC The present invention describes a method (M1) for amplifying a nucleic
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other, and contacting (S) with a
 CC primer having the predetermined sequence in the presence of a polymers
 CC and nucleotides under conditions suitable for polymerisation of the
 CC nucleotides. Also described is an engineered nucleic acid strand (I)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other end. M1 is useful for
 CC amplifying a nucleic acid. M1 can be used for producing an antibody
 CC library. M1 is useful for preparing amplified products that can be
 CC ligated into a suitable expression vector, where the vector can be used
 CC to transform an appropriate host organism to produce the polypeptide or
 CC protein encoded by the target sequence. M1 is useful to amplify a family
 CC of related sequences to build a complex library such as, for example an
 CC antibody library. M1 is useful not only for producing large amounts of
 CC one target nucleic acid sequence, but also for amplifying simultaneously
 CC more than one different target nucleic acid sequence located on the same
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
 CC ABR54998 represent sequence used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 107 AA;
 Query Match 94.8%; Score 527; DB 6; Length 107;
 Best Local Similarity 93.5%; Pred. No. 4.5e-32;
 Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWNPRTFGQTKVEIK 107
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWNPRTFGPGTKVDIK 107
 RESULT 11
 ABR54883
 ID ABR54883 standard; protein; 107 AA.
 AC ABR54883;
 XX
 DT 30-JUN-2003 (first entry)
 XX
 DE Light chain clone HBPAXK1b 3A2 SEQ ID NO:109.
 XX
 KW Engineered template; single primer amplification; antibody library;
 KW nucleic acid amplification.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003025202-A2.
 XX
 XX 27-MAR-2003.
 PD
 XX 19-SEP-2002; 2002WO-US029889.
 PF
 XX 19-SEP-2001; 2001US-0323455P.
 PR
 XX

PA (ALEX-) ALEXION PHARM INC.
 XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
 XX WPI; 2003-313359/30.
 DR
 XX Amplifying nucleic acid by contacting engineered nucleic acid strand
 PT having predetermined sequence at one end and sequence complementary to
 PT predetermined sequence at other end, with primer having predetermined
 PT sequence.
 XX
 PS Example 3; Fig 8b-c; 68pp; English.
 XX
 CC The present invention describes a method (M1) for amplifying a nucleic
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other, and contacting (S) with a
 CC primer having the predetermined sequence in the presence of a polymers
 CC and nucleotides under conditions suitable for polymerisation of the
 CC nucleotides. Also described is an engineered nucleic acid strand (I)
 CC having a predetermined sequence at one end and a sequence complementary
 CC to the predetermined sequence at the other end. M1 is useful for
 CC amplifying a nucleic acid. M1 can be used for producing an antibody
 CC library. M1 is useful for preparing amplified products that can be
 CC ligated into a suitable expression vector, where the vector can be used
 CC to transform an appropriate host organism to produce the polypeptide or
 CC protein encoded by the target sequence. M1 is useful to amplify a family
 CC of related sequences to build a complex library such as, for example an
 CC antibody library. M1 is useful not only for producing large amounts of
 CC one target nucleic acid sequence, but also for amplifying simultaneously
 CC more than one different target nucleic acid sequence located on the same
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
 CC ABR54998 represent sequence used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 107 AA;
 Query Match 94.8%; Score 527; DB 6; Length 107;
 Best Local Similarity 93.5%; Pred. No. 4.5e-32;
 Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWNPRTFGQTKVEIK 107
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWNPRTFGQGRLEIK 107
 RESULT 12
 ADP22404
 ID ADP22404 standard; protein; 107 AA.
 AC ADP22404;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFa antibody light chain variable region SEQ ID NO:310.
 XX
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriasis; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; Graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX

OS Homo sapiens.
 PN WO2004050683-A2.
 PD 17-JUN-2004.
 PP 02-DEC-2003; 2003WO-US038281.
 PR 02-DEC-2002; 2002US-0430729P.
 XX (ABGE-) ABGENIX INC.
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX Example 10; SEQ ID NO 310; 213pp; English.
 XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC the sample; (2) a composition comprising the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody and TNFa in
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiartherosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNPa
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX Sequence 107 AA;
 SQ
 Query Match 94.8%; Score 527; DB 8; Length 107;
 Best Local Similarity 93.5%; Pred. No. 4.5e-32;
 Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNPAWYQQKPGQAPRLIFGASTRATGIPA 60
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSSNLAWYQQKPGQAPRLIFGASTRATGIPA 60
 QY 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGKVK 107
 DB 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGKVK 107

RESULT 13
 ADP22407

ID ADP22407 standard; protein; 107 AA.
 AC ADP22407;
 XX 09-SEP-2004 (first entry)
 DT Human anti-TNPa antibody light chain variable region SEQ ID NO:313.
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 DE anti-TNPa antibody; anabolic; antiartherosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoaric; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX Homo sapiens.
 OS WO2004050683-A2.
 PN 17-JUN-2004.
 PD 02-DEC-2003; 2003WO-US038281.
 XX 02-DEC-2002; 2002US-0430729P.
 PR (ABGE-) ABGENIX INC.
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX Example 10; SEQ ID NO 313; 213pp; English.
 XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC the sample; (2) a composition comprising the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody and TNFa in
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiartherosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNPa
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX Sequence 107 AA;
 SQ

Job time : 62.3676 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds
(without alignments)
805.260 Million cell updates/sec

Title: US-10-660-357A-34
Perfect score: 556
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNWPRTFGGTKVEIK 107
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	96.2	107	2 S34005	Ig kappa chain V r
2	527	94.8	117	2 S40362	Ig kappa chain - h
3	522	93.9	128	2 S40343	Ig kappa chain V-J
4	504.5	90.7	109	1 K3HUPM	Ig kappa chain V-I
5	490.5	88.2	131	2 S40328	Ig kappa chain - h
6	486.5	87.5	116	2 B26555	Ig kappa chain V-I
7	486	87.4	128	2 A56701	Ig kappa chain V r
8	482	86.7	111	2 S23628	Ig kappa chain V r
9	481.5	86.6	215	2 JE0244	Ig kappa chain NIG
10	475	85.4	115	1 K3HUCI	Ig kappa chain pre
11	474	85.3	115	2 A30553	Ig kappa chain pre
12	474	85.3	215	2 JE0243	Ig kappa chain NIG
13	473	85.1	144	2 PL0106	Ig kappa chain pre
14	467.5	84.1	109	2 D30601	Ig kappa chain V-I
15	466.5	83.9	129	1 K3HUIA	Ig kappa chain pre
16	464.5	83.5	109	2 F30607	Ig kappa chain V-I
17	464	83.5	95	2 PH0868	Ig kappa chain V r
18	464	83.5	98	2 S30608	Ig kappa chain V-I
19	463.5	83.4	114	2 S54905	Ig kappa chain V r
20	462	83.1	110	2 S40326	Ig kappa chain V-J
21	462	83.1	123	2 S40378	Ig kappa chain - h
22	462	83.1	128	2 S40379	Ig kappa chain V-J
23	461.5	82.8	109	1 K3HUII	Ig kappa chain V-I
24	460.5	82.8	109	2 B30601	Ig kappa chain V-I
25	460.5	82.8	128	2 S20636	Ig kappa chain V r
26	460.5	82.8	129	2 S42274	Ig kappa chain pre
27	459.5	82.6	109	2 G30601	Ig kappa chain V-I
28	459	82.6	91	2 S37527	Ig kappa chain V r
29	459	82.6	108	2 G44151	Ig kappa chain V r

30	458.5	82.5	109	1 K3HUTI	Ig kappa chain V-I
31	458.5	82.5	110	2 S20635	Ig kappa chain V r
32	457.5	82.3	109	2 H30601	Ig kappa chain V-I
33	457.5	82.3	109	2 S40601	Ig kappa chain V-I
34	457.5	82.3	129	2 S49532	anti-Sm antibody V
35	456.5	82.1	108	2 C30608	Ig kappa chain V-I
36	455.5	81.9	109	2 PH0963	Ig kappa chain V r
37	454.5	81.7	109	1 K3HUIA	Ig kappa chain V-I
38	453.5	81.6	109	2 A30608	Ig kappa chain V-I
39	453.5	81.6	129	1 K3HUII	Ig kappa chain pre
40	450.5	81.0	215	2 JE0242	Ig kappa chain NIG
41	450	80.9	129	2 S29627	Ig kappa chain V r
42	449	80.8	107	2 S57444	Ig kappa chain V-J
43	448.5	80.7	109	2 F30601	Ig kappa chain V-I
44	448	80.6	114	2 S46375	Ig kappa chain V-J
45	447.5	80.5	129	2 S46369	Ig light chain var

ALIGNMENTS

RESULT 1

S34005
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34005; S30524
R:Mariette, X.; Tsapig, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MAR>
A:Cross-references: EMBL:X18330
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 96.2%; Score 535; DB 2; Length 107;
Best Local Similarity 95.3%; Pred. No. 3.3e-39;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY	1	EIVMTQSPATLSVSPGERATLS	CRASQSSINNF	AWYQKPGQAPRLLI	FGASTRATGIPA	60
DB	1	EIVMTQSPATLSVSPGERATLS	CRASQSSVSNL	AWYQKPGQAPRLLI	YGASTRATGIPA	60
QY	61	RPSGSGSGTEFTLTIS	LSQSEDF	AVYVCOQYNNWPR	TFGGTKVEIK	107
DB	61	RPSGSGSGTEFTLTIS	LSQSEDF	AVYVCOQYNNWPR	TFGGTKVEIK	107

RESULT 2

S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40362
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:G441412; PID:G441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 527; DB 2; Length 117;

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Best Local Similarity 94.4%; Pred. No. 1.7e-38; Mismatches 3; Indels 0; Gaps 0;
Matches 101; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIPA 60
Db 11 EIVMTQSPATLSVSPGERATLSCRASQSISSNNLAWYQKPGQAPRLLIYGASTRATGIPA 70
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 71 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPLTFGGTKVEIK 117

RESULT 3
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAAS1121.1; PID:g441375
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 522; DB 2; Length 128;
Best Local Similarity 92.3%; Pred. No. 5.1e-38; Mismatches 3; Indels 0; Gaps 0;
Matches 99; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 80
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 81 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPTTFGGTKLEIK 127

RESULT 4
K3HUPM
Ig kappa chain V-III region (Pom) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01897
R:Klapper, D.G.; Capra, J.D.
Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976
A:Title: The amino acid sequence of the variable regions of the light chains from two id
A:Reference number: A01897
A:Accession: A01897
A:Molecule type: protein
A:Residues: 1-109 <KLA>
C:Cross-references: UNIPROT:P01624
C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;23-89/Disulfide bonds: #status predicted

Query Match 90.7%; Score 504.5; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 1.4e-36; Mismatches 4; Indels 1; Gaps 1;
Matches 98; Conservative
```

```
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIP 59
Db 1 EIVMTQSPVTLISVSPGERATLSCRASQSISSNLAWYQKPGSRLLIYGASTRATGIP 60
QY 60 ARFSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 ARFSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPTTFGGTRVEIK 108

RESULT 5
S40328
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40328
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CAAS1106.1; PID:g441345
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 490.5; DB 2; Length 131;
Best Local Similarity 87.0%; Pred. No. 2.6e-35; Mismatches 6; Indels 1; Gaps 1;
Matches 94; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIPA 60
Db 20 EIVMTQSPATLSVSPGERATLSCRASQSVIHLNLAWYQKPGQAPRLLIYGATRATGVPA 79
QY 61 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 80 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPTTFGGTKVEIK 127

RESULT 6
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Midhaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137686; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 486.5; DB 2; Length 116;
Best Local Similarity 88.0%; Pred. No. 5.1e-35; Mismatches 7; Indels 1; Gaps 1;
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQVPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIYAASRATGIPA 60
QY 61 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYDDWPTTFGGTRLEIK 108

RESULT 7
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Midhaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137686; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 486.5; DB 2; Length 116;
Best Local Similarity 88.0%; Pred. No. 5.1e-35; Mismatches 7; Indels 1; Gaps 1;
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQVPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIYAASRATGIPA 60
QY 61 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGGTEFTLTISLSQSEDFAVYCCQYDDWPTTFGGTRLEIK 108

RESULT 7
```

A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 481.5; DB 2; Length 215;
Best Local Similarity 86.1%; Pred. No. 2.4e-34;
Matches 93; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLISCRASQSIINNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
|:::|||||||:|||||||:|:|||||||:|||||||:
Db 1 EVLTQTSPATLSVSPGERATLISCRASQSVHSLAWYQQKPGQAPRLLIYRASTRATGIPA 60
|:::|||||||:|||||||:|:|||||||:|||||||:

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNWP-PRTEGGQTKVEIK 107
|:::|||||||:|||||||:|:|||||||:|||||||:
Db 61 RFSGSGSGTDPIITLTISLSQSEDFALYYCOQYNTPPLTTEGGGTVKEIK 108
|:::|||||||:|||||||:|:|||||||:|||||||:

RESULT 10
K3HUCL
IG kappa chain precursor V-III region (CLL) - human
N;Alternate names: rheumatoid factor
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C;Accession: A01898
R;Jirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A;Title: Cloning and sequence determination of a human rheumatoid factor light-chain gene
A;Reference number: A01898; PMID:86177570; PMID:3083417
A;Accession: A01898
A;Molecule type: DNA
A;Residues: 1-115 <JIR>
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:I36266
A;Map position: 2p12-2p11
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/Disulfide bonds: #status predicted

Query Match 85.4%; Score 475; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 4.9e-34;
Matches 90; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLISCRASQSIINNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
|:::|||||||:|||||||:|:|||||||:|||||||:
Db 21 EIVMTQSPATLSVSPGERATLISCRASQSVNNLAAYQQKPGQPPRLIYGASTRATGIPA 80
|:::|||||||:|||||||:|:|||||||:|||||||:

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNWP 95
|:::|||||||:|||||||:|:|||||||:|||||||:
Db 81 RFSGSGSGTEFTLTISRLLSQSEDFAVYYCOQYNWP 115
|:::|||||||:|||||||:|:|||||||:|||||||:

RESULT 11
A30553
IG kappa chain precursor V-III region (Hah) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30553

R.; Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.
J. Immunol. 142, 688-694, 1989
A;Title: Characterization of four homologous L chain variable region genes that are rela
A;Reference number: A30553; MUID:89093959; PMID:2492051
A;Accession: A30553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115
A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 474; DB 2; Length 115;
Best Local Similarity 94.7%; Pred.No.5.9e-34;
Matches 90; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAWYQQKPGAPRLIFGCASTRATGIPA 60
Db 21 EIVMQSPATLSVSPGERATLSCRASQSNNLAWYQQKPGAPRLIYGASTRATGIPA 80
Qy 61 RFSGSGGTFTLTISSLQSEDFAVYYCCQYNWP 95
Db 81 RFSGSGGTFTLTISLQSEDFAVYYCCQYNWP 115

RESULT 12
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazai, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 474; DB 2; Length 215;
Best Local Similarity 85.0%; Pred.No.1e-33;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAWYQQKPGAPRLIFGCASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVNVMQLGQAPRLIYDASTRATGPVA 60
Qy 61 RFSGSGGTFTLTISSLQSEDFAVYYCCQYNWPRTFGGTKVEIK 107
Db 61 RFSGSGGTFTLTISLQSEDFAIYYCOHNAWPPTFGGTKRVETK 107

RESULT 13
PL0106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PL0106; MUID:89233583; PMID:2541221
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
F;36-110/Domain: immunoglobulin homology <IMM>

F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <CRE>

Query Match 85.1%; Score 473; DB 2; Length 144;
Best Local Similarity 84.1%; Pred. No. 8.9e-34;
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISINNFAYVYCOQKPGQAPRLLIFFGASTRATGIPA 60
DB 21 EIVLTQSPATLSVSPGERATLSCRASQSVSYLAWYQORPGQAPRLLIYDASNRATGIPA 80
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGGTKEIK 107
DB 81 RFSGSGSGTDFTLTISLSEPFDAVYYCQQRSSNNPLTFGGGTKEIK 127

RESULT 14
D30601
Ig kappa chain V-III region (Cur) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: D30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A;Reference number: A30601; MUID:99215279; PMID:2496160
A;Accession: D30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 467.5; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 2e-33;
Matches 90; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISINNF-AYVYCOQKPGQAPRLLIFFGASTRATGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQORPGQAPRLLIYGASSTRATGIP 60
QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGGTKEIK 107
DB 61 DRFSGSGSGTDFTLTISRLEPDAVYYCQYVGSFRIFGGGTKEIK 108

RESULT 15
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: PL0022
R;Kippes, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0022
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
A;Cross-references: UNIPROT:P18135
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed in
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:I36266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

Query Match 83.9%; Score 466.5; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 2.9e-33;
Matches 90; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIISNNF-AWYQKPGQAPRLLI FGASTRATGIP 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 60 ARFSGSGSGTEFTLTITISQLQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPRTFGGTKVEIK 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 16, 2005, 22:04:10
Job time : 13.7849 secs

THE NEEDS (1979)

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-34

Perfect score: 556

Sequence: 1 BIVMTQSPATLSVSPGERAT.....CQQYNWPRTPGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	515.5	92.7	129	1	KV3H_HUMAN	P04207 homo sapien
2	504.5	90.7	109	1	KV3F_HUMAN	P01624 homo sapien
3	504	90.6	108	2	Q9UL83	Q9ul83 homo sapien
4	498.5	89.7	109	2	Q9UL85	Q9ul85 homo sapien
5	488.5	87.9	235	2	O6GMW0	O6gmw0 homo sapien
6	466.5	83.9	129	1	KV3L_HUMAN	P18135 homo sapien
7	461.5	83.0	109	1	KV3B_HUMAN	P01620 homo sapien
8	458.5	82.5	109	1	KV3D_HUMAN	P01622 homo sapien
9	454.5	81.7	109	1	KV3E_HUMAN	P01623 homo sapien
10	453.5	81.6	129	1	KV3M_HUMAN	P18136 homo sapien
11	445.5	80.1	109	2	Q9UL78	Q9ul78 homo sapien
12	437.5	78.7	109	1	KV3G_HUMAN	P04206 homo sapien
13	435.5	78.3	108	1	KV3A_HUMAN	P01619 homo sapien
14	435.5	78.3	235	2	O6PJF2	O6pjf2 homo sapien
15	430.5	77.4	235	2	O6GMV9	O6gmw9 homo sapien
16	429	77.2	115	1	KV31_HUMAN	P04433 homo sapien
17	428	77.0	128	1	KV3K_HUMAN	P06311 homo sapien
18	428	77.0	236	2	O6PIL8	O6pil8 homo sapien
19	423	76.1	108	1	KV1M_HUMAN	P01605 homo sapien
20	422.5	76.0	109	2	Q9UL86	Q9ul86 homo sapien
21	422	75.9	236	2	O6P5S8	O6p5s8 homo sapien
22	415	74.6	108	2	Q9UL79	Q9ul79 homo sapien
23	411	73.9	134	1	KV4C_HUMAN	P06314 homo sapien
24	409.5	73.7	116	1	KV3J_HUMAN	P04434 homo sapien
25	400	71.9	108	2	Q9UL70	Q9ul70 homo sapien
26	400	71.9	236	2	O6GMW1	O6gmw1 homo sapien
27	399	71.8	114	1	KV4A_HUMAN	P01625 homo sapien
28	398.5	71.7	100	1	KV3C_HUMAN	P01621 homo sapien
29	398	71.6	108	1	KV1R_HUMAN	P01610 homo sapien
30	398	71.6	236	2	O6PIH7	O6pih7 homo sapien
31	398	71.6	236	2	O6PIT5	O6pit5 homo sapien

Query Match

92.7%; Score 515.5; DB 1; Length 129;

32	396	71.2	234	2	Q7Z473	Q7z473 homo sapien
33	395	71.0	108	1	KV1G_HUMAN	P01599 homo sapien
34	393.5	70.8	133	1	KV4B_HUMAN	P06313 homo sapien
35	393	70.7	108	1	KV1F_HUMAN	P01598 homo sapien
36	393	70.7	108	1	KV1V_HUMAN	P04430 homo sapien
37	393	70.7	236	2	O7Z3Y4	Q7z3y4 homo sapien
38	393	70.7	244	2	O6SZC8	Q6szc8 homo sapien
39	390	70.1	108	1	KV1L_HUMAN	P01604 homo sapien
40	389	70.0	236	2	O6GMX8	Q6gmx8 homo sapien
41	388	69.8	240	2	O6SZC9	Q6szc9 homo sapien
42	387	69.6	255	2	O6KB05	Q6kb05 mus musculu
43	386	69.4	108	1	KV1Q_HUMAN	P01609 homo sapien
44	386	69.4	108	1	KV1Y_HUMAN	P80362 homo sapien
45	385	69.2	108	1	KV1H_HUMAN	P01600 homo sapien

ALIGNMENTS

RESULT 1
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M12740; AA58992.1; -
CC HSSP; P01625; ILVE.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region CLL.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 118 Complementarity-determining-3.
FT DOMAIN 119 129 Jk1 segment.
FT DISULFID 43 108 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

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Best Local Similarity 92.6%; Pred. No. 6.1e-48;
Matches 100; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 80
QY 61 RFGSGSGTFTLTITSSQSEDFAVYVCOQYNNWPR-TFGQGTKEVIEK 107
DB 81 RFGSGSGTFTLTITSSQSEDFAVYVCOQYNNWPPFTFGQGTKEVIEK 128

RESULT 2
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive Igm anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
globulin activity.
CC PIR; A01897; K3HUPM.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DPC6A8ABA86 CRC64;

Query Match 90.7%; Score 504.5; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 7.9e-47;
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIIFGASTRATGIP 59
DB 1 EIVMTQSPVTLSPGERATLSCRASQSIINSYAWYQKPGSPRLLIYGASTRATGIP 60
QY 60 ARFSGSGTFTLTITSSQSEDFAVYVCOQYNNWPR-TFGQGTKEVIEK 107
DB 61 ARFSGSGTFTLTITSSQSEDFAVYVCOQYNNWPPFTFGQGTKEVIEK 108

RESULT 3
QYUL83 PRELIMINARY; PRT; 108 AA.
AC QYUL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Best Local Similarity 89.7%; Score 498.5; DB 2; Length 109;
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; D30609; D30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P01625; ILVE.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA968EA CRC64;

Query Match 90.6%; Score 504; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 8.8e-47;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSQSEDFAVYVCOQYNNWPR-TFGQGTKEVIEK 107
DB 61 RFGSGSGTFTLTITSSQSEDFAVYVCOQYNNWPPFTFGQGTKEVIEK 107

RESULT 4
QYUL85 PRELIMINARY; PRT; 109 AA.
AC QYUL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
(fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSSP; P01625; IEK3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 89.7%; Score 498.5; DB 2; Length 109;
Best Local Similarity 90.7%; Pred. No. 3.5e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
```


QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
 Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
 Db 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 108

RESULT 5

Q6GMW0 PRELIMINARY; PRT; 235 AA.
 AC O6GMW0
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B.; Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073792; AAH73792.1; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00385; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 87.9%; Score 488.5; DB 2; Length 235;
 Best Local Similarity 88.0%; Pred. No. 1.1e-44;
 Matches 95; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
 Db 21 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQKPGQAPRLLIIFGASTRATGIP 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
 Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 128

RESULT 6

KV3L_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HAH precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RT J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: The protein is one of the surface immunoglobulin M
 autoantibodies expressed in patients with chronic lymphocytic
 leukemia.
 CC PIR; P10022; K3HUHA.
 DR HSSP; P01625; 1EEQ.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00385; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 Ig kappa chain V-III region HAH.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 55 Complementarity-determining-1.
 FT DOMAIN 56 70 Framework-2.
 FT DOMAIN 71 77 Complementarity-determining-2.
 FT DOMAIN 78 109 Framework-3.
 FT DOMAIN 110 118 Complementarity-determining-3.
 FT DOMAIN 119 129 JkI segment.
 FT DISULFID 43 109 By similarity.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 83.9%; Score 466.5; DB 1; Length 129;
 Best Local Similarity 83.3%; Pred. No. 1.3e-42;
 Matches 90; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNF-AMYQKPGQAPRLLIIFGASTRATGIP 59
 Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSTRATGIP 80
 QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107
 Db 81 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPRTFGQGTKEIK 128

RESULT 7

KV3B_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

```
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3HUSI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 83.0%; Score 461.5; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 3.6e-42;
Matches 88; Conservative 13; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYGASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCYQYNNWPRTFGGTKVEIK 107
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYSGSPSTFGQTKVELK 108

RESULT 8
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUTI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 82.5%; Score 458.5; DB 1; Length 109;
Best Local Similarity 82.4%; Pred. No. 7.7e-42;
Matches 89; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYVASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCYQYNNWPRTFGGTKVEIK 107
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYSGSPSTFGQTKVELK 108

RESULT 9
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01896; K3HJML.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 81.7%; Score 454.5; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 2.1e-41;
Matches 88; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYVASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCYQYNNWPRTFGGTKVEIK 107
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYSGSLGTFGGTKVEIK 108

RESULT 10
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Yosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; H44151; H44151.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0964; PH0964.
DR PIR; PH0965; PH0965.
DR PIR; S33988; S33988.
DR PIR; S34096; S34096.
DR HSSP; P01625; LEK3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; I_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 80.1%; Score 445.5; DB 2; Length 109;
Best Local Similarity 80.6%; Pred. No. 2e-40;
Matches 87; Conservative 11; Mismatches 9; Indels 1; Gaps

QY 1 EIVMTOSPATLSVSGERATLSCRASQTSNNF-AWYQKQGQAPRLLI FGASTRATGIP 59
DB 1 EIVLTOSPATLSVSGERATLSCRASQSSVSLAWYQKQGQAPRLLIY GASSRATGIP 60

QY 60 ARFSGSGSGTFTLTISLSQSDFAVYCCQYNNWPRTFGGQTKVEIK 107
DB 61 DRFSGSGSGTFTLTISRLEPEDCAVYCCQYGGSPLTFGGQTKVEIK 108

RESULT 12
KV3G_HUMAN
ID KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA Newkirk M., Chen P.P., Carson D.A., Fosnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotypic group, in part predicted by its
RT reactivity with anti-peptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).

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DR PIR; A01893; K3HUGO.
DR HSSP; P01625; 1EX3.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 78.7%; Score 437.5; DB 1; Length 109;
Best Local Similarity 78.7%; Pred. No. 1.5e-39;
Matches 85; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNF-AWYQKPGQAPRLIFGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRAALLSRGVLAWYQKPGQAPRLIMYGSSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFLTISRLEPEDFAVYCYQYGSFSPFGQGTKEIK 108

RESULT 13
KV3A HUMAN STANDARD; PRT; 108 AA.
ID AC_KV3A_HUMAN
IC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE.
RA Milstein C.;
RA "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSSP; P01625; 1EEQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 78.3%; Score 435.5; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 2.4e-39;
Matches 81; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNF-AWYQKPGQAPRLIFGASTRATGIP 59
Db 1 ZIVLTZSPGTLSPGZRAALSCRSQSLSGNLYAWYQKPGQAPRLIMYGSSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGADFTLTISRLEPEDFAVYCYQYGSFSPFGQGSKEIK 108
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RESULT 14
Q6PJF2 PRELIMINARY; PRT; 235 AA.
ID AC_Q6PJF2
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 78.3%; Score 435.5; DB 2; Length 235;
Best Local Similarity 78.7%; Pred. No. 5.9e-39;
Matches 85; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNF-AWYQKPGQAPRLIFGASTRATGIP 59
Db 21 EIVLTQSPATLSVSPGERATLSCRSQIVSSAYLAWYQKPGQAPRLIMFGSSSRATGIP 80

QY 60 ARFSGSGSGTEFTLTISLQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
Db 81 DRFSGSGSGTDFLTISRLEPEDFAVYCYQYGSQGTGPGTKVDIK 128

RESULT 15
Q6GMV9
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ID O6GMV9 PRELIMINARY; PRT; 235 AA.
AC O6GMV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 77.4%; Score 430.5; DB 2; Length 235;
Best Local Similarity 76.9%; Pred. No. 2.1e-38;
Matches 83; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNP-ANYQOKPGQAPRLILFGASTRATGIP 59
DB 21 EIVLTQSPGTLSPGERAALSCRASQVNSKYLAWYQKPGQAPRLMYAASIRATGIP 80
QY 60 ARFSGSGSGTEFTLTISSLQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107
DB 81 DRFSGSGSGTFTLTISRLESEDFALYFCQYGTSPLTFTGGTKVEIK 128

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Job time : 59.9908 secs

RECEIVED BY BANK (CSTC)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds
(without alignments)
439.017 Million cell updates/sec

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Perfect score: 556
Sequence: 1 EIVMTSPATLSVSPGERAT.....CQYNNWPTFGQTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520.5	93.6	117	4	US-09-203-768A-4
2	489	87.9	224	4	US-09-456-090A-82
3	489	87.9	224	4	US-09-456-090A-88
4	489	87.9	224	4	US-09-456-090A-90
5	489	87.9	224	4	US-09-453-234-82
6	489	87.9	224	4	US-09-453-234-88
7	489	87.9	224	4	US-09-453-234-90
8	486	87.4	224	4	US-09-456-090A-36
9	486	87.4	224	4	US-09-453-234-36
10	476	85.6	224	4	US-09-456-090A-84
11	476	85.6	224	4	US-09-453-234-84
12	475	85.4	224	4	US-09-456-090A-46
13	475	85.4	224	4	US-09-453-234-46
14	466	83.8	106	4	US-08-635-109-8
15	466	83.8	106	4	US-08-844-215-11
16	465.5	83.7	109	3	US-09-025-769B-16
17	465.5	83.7	109	4	US-09-490-070A-16
18	465.5	83.7	109	4	US-09-490-153-16
19	465.5	83.7	109	4	US-09-490-324-16
20	464.5	83.5	110	3	US-09-025-769B-30
21	464.5	83.5	110	3	US-09-025-769B-47
22	464.5	83.5	110	4	US-09-490-070A-30
23	464.5	83.5	110	4	US-09-490-070A-47
24	464.5	83.5	110	4	US-09-490-153-30
25	464.5	83.5	110	4	US-09-490-153-47
26	464.5	83.5	110	4	US-09-490-324-30
27	464.5	83.5	110	4	US-09-490-324-47

28 462 83.1 234 3 US-09-049-672A-6 Sequence 6, Appli
29 459.5 82.6 235 4 US-09-472-087-14 Sequence 14, Appl
30 459.5 82.6 235 4 US-09-472-087-65 Sequence 65, Appl
31 457.5 82.3 108 2 US-08-232-081B-42 Sequence 42, Appl
32 454.5 81.7 108 1 US-07-634-278-86 Sequence 86, Appl
33 454.5 81.7 108 1 US-08-477-728-86 Sequence 86, Appl
34 454.5 81.7 108 1 US-08-474-040-86 Sequence 86, Appl
35 454.5 81.7 108 1 US-08-487-200-86 Sequence 86, Appl
36 454.5 81.7 108 1 US-08-488-113B-150 Sequence 150, App
37 454.5 81.7 108 2 US-08-477-484B-150 Sequence 150, App
38 454.5 81.7 108 2 US-08-646-360-150 Sequence 150, App
39 454.5 81.7 108 3 US-08-839-765-150 Sequence 150, App
40 454.5 81.7 108 3 US-09-136-389-150 Sequence 150, App
41 454.5 81.7 108 3 US-08-484-537-86 Sequence 86, Appl
42 454.5 81.7 108 3 US-09-610-838-150 Sequence 150, App
43 454.5 81.7 108 4 US-09-711-485-150 Sequence 150, App
44 454 81.7 107 1 US-07-634-278-63 Sequence 63, Appl
45 454 81.7 107 1 US-07-634-278-87 Sequence 87, Appl

ALIGNMENTS

RESULT 1

US-09-203-768A-4

; Sequence 4, Application US/09203768A

; Patent No. 6787638

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods

; TITLE OF INVENTION: of Use

; FILE REFERENCE: P-IX 2947

; CURRENT APPLICATION NUMBER: US/09/203,768A

; CURRENT FILING DATE: 1998-12-02

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-203-768A-4

Query Match 93.6%; Score 520.5; DB 4; Length 117;
Best Local Similarity 93.5%; Pred. No. 5.6e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIVMTSPATLSVSPGERATLSCRASQSSNNFNFWYQKPGQAPRLLIIFGASTRATGIPA 60

DB 9 EIVMTSPATLSVSPGERATLSCRASQSSNNFNFWYQKPGQAPRLLIIFGASTRATGIPA 68

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGTKEIK 107

DB 69 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFQGTKEIK 116

RESULT 2

US-09-456-090A-82

; Sequence 82, Application US/09456090A

; Patent No. 6680209

; GENERAL INFORMATION:

; APPLICANT: Buechler, Joe

; APPLICANT: Valkirs, Gunars

; APPLICANT: Gray, Jeff

; APPLICANT: Lonberg, Nils

; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

; FILE REFERENCE: 020015-00020009

; CURRENT APPLICATION NUMBER: US/09/456,090A

; CURRENT FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 82

; LENGTH: 224

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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
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QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
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Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
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RESULT 4
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
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QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
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Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIIFGASTRATGIPA 60
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
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RESULT 6
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
US-09-453-234-88
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; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAYVQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVVYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVVYCOQNNWPRTFGGTKVEIK 107

RESULT 7
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAYVQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVVYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVVYCOQNNWPRTFGGTKVEIK 107

RESULT 8
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match      87.4%; Score 486; DB 4; Length 224;
Best Local Similarity 86.0%; Pred. No. 1.7e-37;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAYVQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVVYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVVYCOQNNWPRTFGGTKVEIK 107

RESULT 9
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-36
US-09-453-234-36

Query Match      87.4%; Score 486; DB 4; Length 224;
Best Local Similarity 86.0%; Pred. No. 1.7e-37;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAYVQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVVYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVVYCOQNNWPRTFGGTKVEIK 107

RESULT 10
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
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; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match 85.6%; Score 476; DB 4; Length 224;
Best Local Similarity 85.0%; Pred. No. 1.4e-36;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAMVYQKPGQAPRLLIFGASTRATGIPA 60
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRAGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RFGSGSGTEFTLTISLSQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFLTITISLSEDPFAVYCCQNNWPLTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match 85.6%; Score 476; DB 4; Length 224;
Best Local Similarity 85.0%; Pred. No. 1.4e-36;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAMVYQKPGQAPRLLIFGASTRATGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRAGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RFGSGSGTEFTLTISLSQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFLTITISLSEDPFAVYCCQNNWPLTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A

; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-456-090A-46

Query Match 85.4%; Score 475; DB 4; Length 224;
Best Local Similarity 84.1%; Pred. No. 1.8e-36;
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAMVYQKPGQAPRLLIFGASTRATGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVMTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
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QY 61 RFGSGSGTEFTLTISLSQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFLTITISLSEDPFAVYCCQNSNWPPTFGGTKVEIK 107
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RESULT 13
US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match 85.4%; Score 475; DB 4; Length 224;
Best Local Similarity 84.1%; Pred. No. 1.8e-36;
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAMVYQKPGQAPRLLIFGASTRATGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVMTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RFGSGSGTEFTLTISLSQSEDFAVVYCOQYNNWPRTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFLTITISLSEDPFAVYCCQNSNWPPTFGGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-08-635-109-8
; Sequence 8, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
; APPLICANT: Persson, Mats A. A.
; APPLICANT: Allander, Tobias E.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

```
/
/ ADDRESSEE: REED & ROBINS
/ STREET: 285 Hamilton Avenue, Suite 200
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/635,109
/ FILING DATE: 19-APR-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McCracken, Thomas P
/ REGISTRATION NUMBER: 38,548
/ REFERENCE/DOCKET NUMBER: 2300-6146
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 327-3400
/ TELEFAX: (415) 327-3231
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 106 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-635-109-8

Query Match      83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPATLSVSPGERATLSCRASQSIINNFAVYQQKPGQAPRLIFGASTRATGIPARFS 63
Db 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLIYGGNTRATGTPDRFS 62

QY 64 GSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 63 GSGSGTEFTLTITSSLSQSEDFAVYFCQHYSTWPLTFGGGTVKVEFK 106

Search completed: November 16, 2005, 22:07:22
Job time : 19.1939 secs

/
/ ADDRESSEE: REED & ROBINS
/ STREET: 285 Hamilton Avenue, Suite 200
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/635,109
/ FILING DATE: 19-APR-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McCracken, Thomas P
/ REGISTRATION NUMBER: 38,548
/ REFERENCE/DOCKET NUMBER: 2300-6146
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 327-3400
/ TELEFAX: (415) 327-3231
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 106 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-635-109-8

Query Match      83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPATLSVSPGERATLSCRASQSIINNFAVYQQKPGQAPRLIFGASTRATGIPARFS 63
Db 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLIYGGNTRATGTPDRFS 62

QY 64 GSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 63 GSGSGTEFTLTITSSLSQSEDFAVYFCQHYSTWPLTFGGGTVKVEFK 106

RESULT 15
US-08-844-215-11
/ Sequence 11, Application US/08844215
/ Patent No. 6747136
/ GENERAL INFORMATION:
/ APPLICANT: PERSON, MATS AXEL
/ APPLICANT: ALLANDER, TOBIAS ERIK
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
/ TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ROBINS & ASSOCIATES
/ STREET: 90 MIDDLEFIELD ROAD, SUITE 200
/ CITY: MENLO PARK
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/844,215
/ FILING DATE: 17-APR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/635,109
/ FILING DATE: 19-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MCCracken, THOMAS P.
/ REGISTRATION NUMBER: 38,548
/ REFERENCE/DOCKET NUMBER: 80146.002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 325-7812
/ TELEFAX: (650) 325-7823
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 106 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-844-215-11

Query Match      83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPATLSVSPGERATLSCRASQSIINNFAVYQQKPGQAPRLIFGASTRATGIPARFS 63
Db 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLIYGGNTRATGTPDRFS 62

QY 64 GSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 63 GSGSGTEFTLTITSSLSQSEDFAVYFCQHYSTWPLTFGGGTVKVEFK 106

Search completed: November 16, 2005, 22:07:22
Job time : 19.1939 secs
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המחלקה לבריאות הציבור
המחלקה לבריאות הציבור

Result No.	Query #	Query			DB	ID	Description
		Score	Match	Length			
1	556	100.0	107	14	US-10-330-613-34	Sequence 34, Appl	
2	556	100.0	107	14	US-10-330-530-34	Sequence 34, Appl	
3	556	100.0	107	16	US-10-660-357-34	Sequence 34, Appl	
4	546	98.2	107	14	US-10-330-613-6	Sequence 6, Appl	
5	546	98.2	107	14	US-10-330-530-6	Sequence 6, Appl	
6	546	98.2	107	16	US-10-660-357-6	Sequence 6, Appl	
7	534	96.0	107	15	US-10-251-085B-122	Sequence 122, App	
8	534	96.0	107	15	US-10-737-252-122	Sequence 122, App	
9	530	95.3	107	15	US-10-251-085B-126	Sequence 126, App	
10	530	95.3	107	16	US-10-737-253-126	Sequence 126, App	
11	527	94.8	107	15	US-10-251-085B-109	Sequence 109, App	

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US-10-330-530-34
; Sequence 34, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-34

Query Match      100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107

RESULT 3
US-10-660-357-34
; Sequence 34, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-34

Query Match      100.0%; Score 556; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107

RESULT 4
US-10-330-613-6
; Sequence 6, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-6

Query Match      98.2%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107

RESULT 5
US-10-330-530-6
; Sequence 6, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-6

Query Match      98.2%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107

RESULT 6
US-10-660-357-6
; Sequence 6, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
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; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-6

Query Match 98.2%; Score 546; DB 16; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

DB 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 7

US-10-251-085B-122

; Sequence 122, Application US/10251085B

; Publication No. US20040072164A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Frederickson, Shana

; APPLICANT: Renshaw, Mark

; APPLICANT: Lin, Ying-Chi

; APPLICANT: Maruyama, Toshiaki

; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

; FILE REFERENCE: 1087-21

; CURRENT APPLICATION NUMBER: US/10/251,085B

; CURRENT FILING DATE: 2002-09-19

; PRIOR APPLICATION NUMBER: US 60/323,455

; PRIOR FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 278

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 122

; LENGTH: 107

; TYPE: PRT

; ORGANISM: human

US-10-251-085B-122

Query Match 96.0%; Score 534; DB 15; Length 107;

Best Local Similarity 95.3%; Pred. No. 1.1e-38;

Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

DB 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 8

US-10-737-252-122

; Sequence 122, Application US/10737252

; Publication No. US20040175736A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Frederickson, Shana

; APPLICANT: Renshaw, Mark

; APPLICANT: Lin, Ying-Chi

; APPLICANT: Maruyama, Toshiaki

; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

; FILE REFERENCE: 1087-21 CIP

; CURRENT APPLICATION NUMBER: US/10/737,252

; CURRENT FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-122

Query Match 96.0%; Score 534; DB 16; Length 107;

Best Local Similarity 95.3%; Pred. No. 1.1e-38;

Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

DB 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 9

US-10-251-085B-126

; Sequence 126, Application US/10251085B

; Publication No. US20040072164A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Frederickson, Shana

; APPLICANT: Renshaw, Mark

; APPLICANT: Lin, Ying-Chi

; APPLICANT: Maruyama, Toshiaki

; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

; FILE REFERENCE: 1087-21

; CURRENT APPLICATION NUMBER: US/10/251,085B

; CURRENT FILING DATE: 2002-09-19

; PRIOR APPLICATION NUMBER: US 60/323,455

; PRIOR FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 278

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 126

; LENGTH: 107

; TYPE: PRT

; ORGANISM: human

US-10-251-085B-126

Query Match 95.3%; Score 530; DB 15; Length 107;

Best Local Similarity 94.4%; Pred. No. 2.5e-38;

Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

DB 61 RFGSGSGTEFTLTITSSLOSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 10

US-10-737-252-126

; Sequence 126, Application US/10737252

; Publication No. US20040175736A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Frederickson, Shana

; APPLICANT: Renshaw, Mark

; APPLICANT: Lin, Ying-Chi

; APPLICANT: Maruyama, Toshiaki

; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

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; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-126

Query Match          95.3%; Score 530; DB 16; Length 107;
Best Local Similarity 94.4%; Pred. No. 2.5e-38;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107

RESULT 11
US-10-251-085B-109
; Sequence 109, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-109

Query Match          94.8%; Score 527; DB 15; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKRLEIK 107

RESULT 12
US-10-251-085B-123
; Sequence 123, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark

```

```

; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-123

Query Match          94.8%; Score 527; DB 15; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVDIK 107

RESULT 13
US-10-737-252-109
; Sequence 109, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-109

Query Match          94.8%; Score 527; DB 16; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKRLEIK 107

RESULT 14
US-10-737-252-123
; Sequence 123, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:

```


; APPLICANT: Bowdiah, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
; US-10-737-252-123

Query Match 94.8%; Score 527; DB 16; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTOSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVMTOSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
QY 61 RFSGSGSGTFTLTITSSLSQSEDFAVYVCOQYNNWPRTFGGKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLSQSEDFAVYVCOQYNNWPRTFGGKVEIK 107

RESULT 15

US-10-727-155-310
; Sequence 310, Application US/10727155
; Publication No. US2005004902A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-727-155-310

Query Match 94.8%; Score 527; DB 17; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTOSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVMTOSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
QY 61 RFSGSGSGTFTLTITSSLSQSEDFAVYVCOQYNNWPRTFGGKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLSQSEDFAVYVCOQYNNWPRTFGGKVEIK 107

Search completed: November 16, 2005, 23:05:45
Job time : 66.6949 secs

1111 1111 1111 (1111)

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.2353 Seconds
(without alignments)
674.351 Million cell updates/sec

Title: US-10-660-357A-38

Perfect score: 580

Sequence: 1 DIVWTQSPSLPVIQEPAS.....CMQALQIPITFGGTVKEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	100.0	112	7	ADC99809 Anti-huma
2	580	100.0	112	7	ADD05413 Anti-MUC1
3	580	100.0	112	7	ADF09851 Human ant
4	552	95.2	112	6	ABR55794 Kappa cha
5	552	95.2	112	6	ABR55786 Kappa cha
6	552	95.2	112	7	ADP03893
7	548	94.5	262	5	ABP46070 Human Bly
8	548	94.5	262	7	ADG36897 Single ch
9	547	94.3	112	7	ADP03892 Murine-ex
10	546	94.1	239	3	AAY82615 Human PTH
11	545	94.0	112	6	ABR55770 Kappa cha
12	544	93.8	112	6	ABR55812 Kappa cha
13	544	93.8	112	8	ADI22119 Anti-plat
14	544	93.8	112	6	ADI22122 Anti-plat
15	540	93.1	112	6	ABR55796 Kappa cha
16	540	93.1	112	8	ADL93576 Human CD4
17	540	93.1	238	8	ADL93653
18	539.5	93.0	111	7	ADK18830 Anti-huma
19	539.5	93.0	111	7	ADK18796 Anti-huma
20	539.5	93.0	111	7	ADK18592 Anti-huma
21	539.5	93.0	111	7	ADK18855 Anti-huma
22	539.5	93.0	111	8	ADL25402 Human mab
23	539	92.9	112	8	ADL93564 Human CD4
24	539	92.9	238	8	ADL93649 Human CD4
25	538	92.8	112	7	ADJ76892 Anti-IGF-

ALIGNMENTS

RESULT 1

ADC99809

ID ADC99809 standard; protein; 112 AA.

AC ADC99809;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 38.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX

OS Homo sapiens.

XX

PN WO2003057838-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J;

XX

WPI; 2003-587113/55.

DR N-PSDB; ADC99811.

DR

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

XX

PT or condition associated with expression of MUC18 in a patient, e.g.

XX

PS tumors, cancers, and other malignancies.

XX

Claim 3; SEQ ID NO 38; 78pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.
 XX
 SQ Sequence 112 AA;

Query Match
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 2
 ADD05413
 ID ADD05413 standard; protein; 112 AA.
 XX
 AC ADD05413;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 38.
 XX
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 XX antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057006-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041582.
 XX
 PR 28-DEC-2001; 2001US-0346460P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J, Bar-Eli M;
 XX
 DR WPI; 2003-577496/54.
 DR N-PSDB; ADD05415.
 XX
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.
 XX
 Claim 3; SEQ ID NO 38; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123
 CC amino acids given in the specification, and where the monoclonal antibody
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC sequence represents an anti-MUC18 antibody light chain, variable region,
 CC protein of the invention.

XX
 SQ Sequence 112 AA;

Query Match
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 3
 ADF09851
 ID ADF09851 standard; protein; 112 AA.
 XX
 AC ADF09851;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human anti-MUC18 monoclonal antibody light chain #10.
 XX
 KW cell proliferation inhibition; MUC18 tumour antigen;
 XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 KW carcinoma; cancer; malignancy; light chain; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057837-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041580.
 XX
 PR 28-DEC-2001; 2001US-0346414P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas J;
 XX
 DR WPI; 2003-598367/56.
 DR N-PSDB; ADF09853.
 XX
 XX Inhibiting cell proliferation associated with expression of MUC18 tumor
 PT antigen, involves incubating and inhibiting cell by administering anti-
 PT MUC18 monoclonal antibody.
 XX
 Claim 3; SEQ ID NO 38; 83pp; English.

The invention comprises a method for inhibiting cell proliferation
 CC associated with expression of MUC18 tumour antigen. The method involves
 CC administering anti-MUC18 monoclonal antibody. The method of the invention
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
 CC proliferation associated with the expression of MUC18 tumour antigen, the
 CC method is preferably useful for inhibiting tumour metastasis. The method
 CC is useful for inhibiting cell proliferation in patients with tumours,
 CC carcinomas, cancer and other malignancies. The present amino acid
 CC sequence represents a light chain from an MUC18 tumour antigen-specific
 CC monoclonal antibody.

XX
 SQ Sequence 112 AA;

Query Match
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

Db 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQIPLTFGGTKVEIK 112

RESULT 4
ABR55794
ID ABR55794 standard; protein; 112 AA.
AC ABR55794;
XX
XX
XX 02-SEP-2003 (first entry)
DT
DE Kappa chain variable region of anti-Ang-2 antibody 551 kappa.
XX
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
XX Homo sapiens.
XX

Key Location/Qualifiers
FH Region 23..40
FT /note= "complementarity determining region (CDR) 1"
FT Region 54..62
FT /note= "complementarity determining region (CDR) 2"
FT Region 93..102
FT /note= "complementarity determining region (CDR) 3"
XX
XX WO2003030833-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032613.
XX
XX 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX
XX (AMGE-) AMGEN INC.
XX
XX Oliner JD;
XX
XX WPI; 2003-504963/47.
XX
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
XX Claim 1; Page 93; 161pp; English.

The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55794-830) or its fragment. The binding agents are antibodies that recognize and bind to angiotensin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioma, arteriosclerosis, atherosclerosis, inflammatory disease, inflammatory disorders, atherosclerosis, endometriosis, neoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a kappa chain variable region of an anti-Ang-2 antibody

XX
SQ Sequence 112 AA;

Query Match 95.2%; Score 552; DB 6; Length 112;
Best Local Similarity 94.6%; Pred.No. 2.3e-41;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPVGPAPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
|||||
Db 1 DIVMTQSLPLVPVGPAPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
|||||

QY 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQIPLTFGGTKVEIK 112
|||||

RESULT 5
ABR55786
ID ABR55786 standard; protein; 112 AA.
XX
XX ABR55786;
XX
XX 02-SEP-2003 (first entry)
DT
DE Kappa chain variable region of anti-Ang-2 antibody 543 kappa.
XX
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
XX Homo sapiens.
XX

Key Location/Qualifiers
FH Region 23..40
FT /note= "complementarity determining region (CDR) 1"
FT Region 54..62
FT /note= "complementarity determining region (CDR) 2"
FT Region 93..102
FT /note= "complementarity determining region (CDR) 3"
XX
XX WO2003030833-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032613.
XX
XX 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX
XX (AMGE-) AMGEN INC.
XX
XX Oliner JD;
XX
XX WPI; 2003-504963/47.
XX
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
XX Claim 1; Page 93; 161pp; English.

The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55786-830) or its fragment. The binding agents are antibodies that recognize and bind to angiotensin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioma, arteriosclerosis, atherosclerosis, inflammatory disease, inflammatory disorders, atherosclerosis, endometriosis, neoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a kappa chain variable region of an anti-Ang-2 antibody

XX
SQ Sequence 112 AA;

Query Match 95.2%; Score 552; DB 6; Length 112;
Best Local Similarity 94.6%; Pred.No. 2.3e-41;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPVGPAPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
|||||
Db 1 DIVMTQSLPLVPVGPAPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
|||||

QY 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQIPLTFGGTKVEIK 112
|||||

AAy82615
ID RAY82615 standard; protein; 239 AA.
AC RAY82615;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.
XX
DE Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
KW antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 155
FT /note= "possible Ala"
XX
PN JP2000080100-A.
XX
PD 21-MAR-2000.
XX
PF 12-OCT-1998; 98JP-00304793.
XX
PR 17-JUN-1998; 98JP-00188196.
PR 26-JUN-1998; 98JP-00196729.
XX
PA (NIBS) JAPAN TOBACCO INC.
XX
DR WPI; 2000-286723/25.
DR N-PSDB; AAA13925.
XX
PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain.
XX
PS Claim 31; Page 45-46; 88pp; Japanese.
XX
CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment of
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a human
CC PTHrP monoclonal antibody clone protein sequence from the present
CC invention
XX
SQ Sequence 239 AA;
Query Match 94.1%; Score 546; DB 3; Length 239;
Best Local Similarity 93.8%; Pred. No. 1.8e-40;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIWVTQSPSLPVTGPEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60
DB 21 DIWVTQSPSLPVTGPEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 80
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGIYVCQALQIPLTFGGGKVKIK 112
DB 81 SGVPDRFSGSGGTDFTLKISRVEADVGIYVCQALQIPLTFGGGKVKIK 132
RESULT 11
ABR55770
ID ABR55770 standard; protein; 112 AA.

ABR55770;
XX
DT 02-SEP-2003 (first entry)
XX
DE Kappa chain variable region of anti-Ang-2 antibody 526 kappa.
XX
KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 23..46
FT /note= "complementarity determining region (CDR) 1"
FT Region 54..62
FT /note= "complementarity determining region (CDR) 2"
FT Region 93..102
FT /note= "complementarity determining region (CDR) 3"
XX
PN W02003030833-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032613.
XX
PR 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX
PA (AMGE-) AMGEN INC.
XX
PI Oliner JD;
XX
DR WPI; 2003-504963/47.
XX
PT New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
PS Claim 1; Page 93; 161pp; English.
XX
CC The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a kappa chain variable region of an anti-Ang-2
CC antibody
XX
SQ Sequence 112 AA;
Query Match 94.0%; Score 545; DB 6; Length 112;
Best Local Similarity 93.8%; Pred. No. 9.7e-41;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIWVTQSPSLPVTGPEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60
DB 1 DIWVTQSPSLPVTGPEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGIYVCQALQIPLTFGGGKVKIK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEADVGIYVCQALQIPLTFGGGKVKIK 112
RESULT 12
ABR55812

PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

PS Claim 1; Page 93; 161pp; English.

XX
CC The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABRS5769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity, or
CC haemangioma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, arteriosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a kappa chain variable region of an anti-Ang-2
CC antibody

Sequence 112 AA;

Query Match	93.1%	Score 540;	DB 6;	Length 112;
Best Local Similarity	92.0%;	Pred. No. 2.7e-40;		
Matches 103; Conservative	4;	Mismatches 5;	Indels 0;	Gaps 0;

QY 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNNGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

Db 1 DIWQTSPSLPVTTPGEPASISCRSSOSLLHSGNVDWYLOKPGOSPOLLIIYLSNRA 60

QY 61 SGVPDRFSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112

61 SGVPDRFTGSGSATDFTLRISRVEAEDGVVYCMOALOTPLTFGGGTVKEIK 112

Search completed: November 16, 2005, 21:51:43
Job time : 64.2353 secs

NO PAGE 01 11 2011

Best Local Similarity 93.8%; Pred. No. 1.3e-45;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVPEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVPEPASISCRSSQSLHSGNYNYFDWYLOKPGSQSPQLLIYLGNSRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
DB 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112

RESULT 3
S59207
IG kappa chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58207
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-112 <HEL>
A:Cross-references: EMBL:X99056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 112;
Best Local Similarity 92.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVPEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVPEPASISCRSSQSLHSGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
DB 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112

RESULT 4
S26882
IG kappa chain V region (V607) - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882; MUID:90370099; PMID:2118596
A:Accession: S26882
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 132;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVPEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
DB 21 DIVMTQSPSLPVPVPEPASISCRSSQSLHSGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 80

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
DB 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112

RESULT 5
S40342
IG kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:g441372; PID:g441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;29-108/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVPEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
DB 14 DIVMTQSPSLPVPVPEPASISCRSSQSLHSGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 73

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
DB 74 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 125

RESULT 6
S40357
IG kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 136;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVPEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
DB 21 DIVMTQSPSLPVPVPEPASISCRSSQSLHSGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 80

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
DB 81 SGVPRFSGSGGTDFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 132

RESULT 7
K2HUGM
IG kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A01889; B24452
R/Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A/Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.

A/Reference number: A01889; MUID:84191506; PMID:6325927

A/Accession: A01889

A/Molecule type: mRNA

A/Residues: 1-117 <KLO>

A/Cross-references: UNIPROT:P06309

A/Note: the sequence was determined from the differentiated gene

C/Genetics:

A/Gene: GDB:IGKV2

A/Cross-references: GDB:136265

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>

F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>

F:20-99/Domain: immunoglobulin homology <IMM>

F:27-97/Disulfide bonds: #status predicted

Query Match 90.7%; Score 526; DB 1; Length 117;
Best Local Similarity 91.1%; Pred. No. 1.7e-43;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

DB 5 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 64

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

DB 65 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 116

RESULT 8

S40339

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40339

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40339; MUID:94080891; PMID:8258341

A/Accession: S40339

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-126 <KLE>

A/Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:31-110/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 519.5; DB 2; Length 126;
Best Local Similarity 91.1%; Pred. No. 7.9e-43;
Matches 102; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

DB 16 DIVMTQSPSLPVPVGPGEPAISICRSQSLLHNGYLDWYLOKPGQSPQLLIYLGSNRA 75

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

DB 76 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 126

RESULT 9

K2HUTW

Ig kappa chain V-II region (Mil) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Accession: A01887

R/Dreyer, W.J.; Gray, W.R.; Hood, L.

Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967

A/Title: The genetic, molecular, and cellular basis of antibody formation: some facts and

A/Reference number: A01887

A/Accession: A01887

A/Molecule type: protein

A/Residues: 1-112 <DRE>

A/Cross-references: UNIPROT:P01616

A/Note: the C region of this chain has the Inv (3) marker

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGKV2

A/Cross-references: GDB:136265

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 88.4%; Score 512.5; DB 1; Length 112;
Best Local Similarity 83.9%; Pred. No. 3.2e-42;
Matches 94; Conservative 14; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

DB 1 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 59

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

DB 60 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 111

RESULT 10

S40372

Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40372

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40372

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-131 <KLE>

A/Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 505; DB 2; Length 131;
Best Local Similarity 86.5%; Pred. No. 2e-41;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVGPGEPAISICRSQSLLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

DB 21 DIVMTQSPSLPVPVGPGEPAISICRSQSLLHNGYLDWYLOKPGQSPQLLIYLGSTRA 80

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 111

DB 81 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 131

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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 62.7941 Seconds
(without alignments)
913.348 Million cell updates/sec

Title: US-10-660-357A-38

Perfect score: 580

Sequence: 1 DIVMTQSPSLPVIPEPAS.....CMQALQIPITFGGTRKVIK 112

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	527	90.9	239	2	Q8NEK0	Q8nek0 homo sapien
2	526	90.7	117	1	KV2E_HUMAN	P06309 homo sapien
3	512.5	88.4	112	1	KV2C_HUMAN	P01616 homo sapien
4	502.5	86.6	240	2	Q6PIH6	Q6pih6 homo sapien
5	501	86.4	113	1	KV2D_HUMAN	P01617 homo sapien
6	474.5	81.8	115	1	KV2A_HUMAN	P01614 homo sapien
7	456	78.6	248	2	Q6S2Q7	Q6s2q7 mus sp. b3 (
8	455	78.4	113	1	KV2B_HUMAN	P01615 homo sapien
9	455	78.4	113	1	KV2G_MOUSE	P01631 mus musculus
10	444	76.6	133	1	KV2F_HUMAN	P06310 homo sapien
11	444	76.6	219	2	Q6S2C0	Q6s2c0 mus musculus
12	440	75.9	239	2	Q6F491	Q6f491 homo sapien
13	439	75.7	239	2	Q8TCD0	Q8tcd0 homo sapien
14	429	74.0	113	1	KV2F_MOUSE	P01630 mus musculus
15	427	73.6	114	1	KV2E_MOUSE	P03976 mus musculus
16	426.5	73.5	114	2	Q9UL80	Q9ul80 homo sapien
17	424	73.1	112	2	Q6LEM8	Q6lem8 mus musculus
18	420	72.4	112	1	KV2D_MOUSE	P01629 mus musculus
19	406	70.0	113	1	KV2C_MOUSE	P01628 mus musculus
20	404	69.7	112	1	KV2A_MOUSE	P01626 mus musculus
21	397.5	68.5	108	1	KV1_CANFA	P01618 canis famil
22	387.5	66.8	134	1	KV4C_HUMAN	P06314 homo sapien
23	385	66.4	133	1	KV4B_HUMAN	P06313 homo sapien
24	378.5	65.3	114	1	KV4A_HUMAN	P01625 homo sapien
25	376.5	64.9	255	2	Q6KB05	Q6kb05 mus musculus
26	374	64.5	109	2	Q9UL78	Q9ul78 homo sapien
27	371	64.0	120	1	KV2B_MOUSE	P01627 mus musculus
28	365	62.9	109	1	KV3B_HUMAN	P01620 homo sapien
29	365	62.9	235	2	Q6GKV9	Q6gmV9 homo sapien
30	364	62.8	109	1	KV3D_HUMAN	P01622 homo sapien
31	362.5	62.5	111	1	KV3H_MOUSE	P01660 mus musculus

32	359.5	62.0	111	2	Q920E9	Q920e9 mus musculus
33	359	61.9	129	1	KV3L_HUMAN	P18135 homo sapien
34	358.5	61.8	111	1	KV3R_MOUSE	P01370 mus musculus
35	357.5	61.6	111	1	KV3U_MOUSE	P01673 mus musculus
36	357	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
37	356.5	61.5	111	1	KV3J_MOUSE	P01662 mus musculus
38	356.5	61.5	111	1	KV3S_MOUSE	P01671 mus musculus
39	355.5	61.3	131	1	KV3I_MOUSE	P01661 mus musculus
40	355	61.2	109	1	KV3E_HUMAN	P01623 homo sapien
41	353.5	60.9	109	1	KV4D_HUMAN	P83593 homo sapien
42	353.5	60.9	111	1	KV3K_MOUSE	P01663 mus musculus
43	353.5	60.9	111	1	KV3L_MOUSE	P01664 mus musculus
44	352.5	60.8	111	1	KV3C_MOUSE	P01656 mus musculus
45	352.5	60.8	111	1	KV3N_MOUSE	P01666 mus musculus

ALIGNMENTS

RESULT 1

Q8NEK0 PRELIMINARY; PRT; 239 AA.

AC Q8NEK0;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RA Strausberg R.;
DR Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; I1172.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 90.9%; Score 527; DB 2; Length 239;
Best Local Similarity 91.1%; Pred. No. 5.8e-47;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRA 80
QY 61 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQALQIPLTFGGGKVEIK 112
DB 81 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQGLQTPQTFGGGKVEIK 132

RESULT 2
KV2C HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).

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DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 1
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.
FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 90.7%; Score 526; DB 1; Length 117;
Best Local Similarity 91.1%; Pred. No. 3.1e-47;

Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 5 DIVMTQSPVLPVTPGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRA 64
QY 61 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQALQIPLTFGGGKVEIK 112
DB 65 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQGLQTPQTFGGGKVEIK 116

RESULT 3
KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 88.4%; Score 512.5; DB 1; Length 112;
Best Local Similarity 83.9%; Pred. No. 7.7e-46;
Matches 94; Conservative 14; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPVLPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVLTQSPVLPVTPGEPASISCRSSQSLHSGNYLDWYLOKPGSPZLLIYLGSNRA 59
QY 61 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQALQIPLTFGGGKVEIK 112
DB 60 SGVDPFRFSGSGGTDTFLTKISRVAEADVGIYCMQGLQTPQTFGGGKVEIK 111

RESULT 4
Q6PIH6 PRELIMINARY; PRT; 240 AA.
ID Q6PIH6
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RP "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034142; AAH34142.1; -;
 DR HSSP; P01837; 1KB5.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.C1.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.V.
 DR Pfam; PF07654; C1-set; I.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 240 AA; 26234 MW; 18804D08BB781EC4 CRC64;
 Query Match 86.6%; Score 502.5; DB 2; Length 240;
 Best Local Similarity 87.6%; Pred. No. 2.2e-44;
 Matches 99; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
 QY 1 DIVMTQSLPLSVIPGEPASISCRSSQSLQSGNGNNDYLDWYLOKPGQSPQLLIYLSNRA 60
 DB 21 DIVMAQSPSLSVIPGEPASISCRSSQSLQSGNGNNDYLDWYLOKPGQSPQLLIYLSNRA 80
 QY 61 SGVPRFRSGSGGTDTLTKISRVEADDVGIIYCMQALQI-PLTFGGGKVEIK 112
 DB 81 SGVPRFRSGSGGTDTLTKISRVEADDVGIIYCMQALQTPPYTFGGGKLEIK 133
 RESULT 5
 KV2D HUMAN
 ID KV2D HUMAN STANDARD; PRT; 113 AA.
 AC P01617;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region TEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of
 RT primary amyloidosis.";
 RL Biochemistry 12:3763-3780 (1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
 RA Glenner G.G.;
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a
 RT patient with plasma cell dyscrasia and amyloidosis.";
 RL J. Clin. Invest. 52:1276-1281 (1973).
 CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical
 CC with the Bence Jones protein isolated from the same patient.
 CC -!- MISCELLANEOUS: This protein was isolated from the urine of a
 CC patient with plasma cell dyscrasia and amyloidosis.
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC PIR; A90370; K2HUTW.
 DR HSSP; Q99M37; 1191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; F:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Amyloid; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;
 Query Match 86.4%; Score 501; DB 1; Length 113;
 Best Local Similarity 84.8%; Pred. No. 1.3e-44;
 Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIVMTQSLPLSVIPGEPASISCRSSQSLQSGNGNNDYLDWYLOKPGQSPQLLIYLSNRA 60
 DB 1 DIVMTQSLPLSVIPGEPASISCRSSQSLQSGNGNNDYLDWYLOKPGQSPQLLIYLSNRA 60
 QY 61 SGVPRFRSGSGGTDTLTKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112
 DB 61 SGVPRFRSGSGGTDTLTKISRVEADDVGIIYCMQALQAPITFGGQTRLEIK 112
 RESULT 6
 KV2A HUMAN
 ID KV2A HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region Cum.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE.
 RX MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;

"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [2]

RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE=70063440; PubMed=4188189;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation.";
 RL Naturwissenschaften 56:195-205(1969).
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; B91639; K2HUCM.
 DR HSSP; P01751; INQB.

DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DISULFID 24 95 By similarity.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 81.8%; Score 474.5; DB 1; Length 115;
 Best Local Similarity 82.3%; Pred. No. 7.7e-42;
 Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYLGSKR 59
 DB 2 DIVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYLTLSR 61

QY 60 ASGVPRFSGSGSGTDTFTLKISRVEADDDVGIYYCMAQLQIPLTFGGGTQKVEIK 112
 DB 62 ASGVPRFSGSGSGTDTFTLKISRVAEDVGVIYCMQRLPIPTFGGTQKLEIR 114

RESULT 7
 Q65ZQ7 PRELIMINARY; PRT; 248 AA.
 ID Q65ZQ7
 AC Q65ZQ7
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE B3(Fv)-PE40 (Fragment).
 GN Name=B3(Fv)-PE40;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92020904; PubMed=1924323;
 RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
 RT "regression of a human carcinoma in mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
 DR EMBL; S57990; AAB19971.2; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON TER 248 248
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 78.6%; Score 456; DB 2; Length 248;
 Best Local Similarity 75.9%; Pred. No. 1.7e-39;

Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DIVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYLGSKR 60
 DB 136 DIVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYKVSNR 195
 QY 61 SGVPRFSGSGSGTDTFTLKISRVEADDDVGIYYCMAQLQIPLTFGGGTQKVEIK 112
 DB 196 SGVPRFSGSGSGTDTFTLKISRVEADDDVGIYYCMAQLQIPLTFGGGTQKVEIK 247

RESULT 8
 KV2B HUMAN
 ID KV2B HUMAN STANDARD; PRT; 113 AA.
 AC P01615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region FR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=76253627; PubMed=821524;
 RA Riessen W.F., Jaton J.-C.;
 RT "Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
 RL Biochemistry 15:3829-3833(1976).
 CC -I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.

PIR; A01886; K2HUPR.
 DR HSSP; Q99M37; I191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 39 Complementarity-determining-1.
 FT DOMAIN 40 54 Framework-2.
 FT DOMAIN 55 61 Complementarity-determining-2.
 FT DOMAIN 62 93 Framework-3.
 FT DOMAIN 94 102 Complementarity-determining-3.
 FT DOMAIN 103 112 Framework-4.
 FT DISULFID 23 93 By similarity.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB968E CRC64;

Query Match 78.4%; Score 455; DB 1; Length 113;
 Best Local Similarity 75.0%; Pred. No. 8.3e-40;
 Matches 84; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYLGSKR 60
 DB 1 DVVMTQSPPLSPVTPGEPAISICRSSLQSLQSGNNYLDWYLPKPGQSPQLLIYLSYRD 60
 QY 61 SGVPRFSGSGSGTDTFTLKISRVEADDDVGIYYCMAQLQIPLTFGGGTQKVEIK 112
 DB 61 SGVPRFSGSGSGTDTFTLKISRVAEDVGVIYCMQATZSPYTFGGGTQKLEIK 112

RESULT 9
 KV2G MOUSE
 ID KV2G_MOUSE STANDARD; PRT; 113 AA.
 AC P01631;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE IG kappa chain V-II region 26-10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83178921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 RT anti-digoxin hybridoma antibody."
 RL Biochemistry 22:1153-1158(1983).
 CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
 CC protein that binds digoxin.
 CC PIR; A01914; KVMG26.
 DR HSSP; Q99M37; 1191.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
 KW Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 39 Complementarity-determining-1.
 FT DOMAIN 40 54 Framework-2.
 FT DOMAIN 55 61 Complementarity-determining-2.
 FT DOMAIN 62 93 Framework-3.
 FT DOMAIN 94 102 Complementarity-determining-3.
 FT DOMAIN 103 112 Framework-4.
 FT DISULFID 23 93 By similarity.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

 Query Match 78.4%; Score 455; DB 1; Length 113;
 Best Local Similarity 77.7%; Pred. No. 8.3e-40;
 Matches 87; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

 QY 1 DIVMTQSPSLSPVIGPEPASISCRSSQSLQSGNNYLDWYLQKPGQSPQLLIYLGNSRA 60
 Db 1 DVMTQSPSLSPVIGDQASISCRSSQSLVHSGNTYLNWYLQKAGQSPKLLIYKVSNR 60

 QY 61 SGVPRDFSGSGGTDTLTKISRVEADVGIYCYMQALQIPLTFGGGTKEIK 112
 Db 61 SGVPRDFSGSGGTDTLTKISRVEADLGIYFCSQTHVPTTFGGGTKEIK 112

 RESULT 10
 KV2F HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Kloebeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III."
 RL Nucleic Acids Res. 13:6499-6513(1985).
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 CC -----
 DR EMBL; Z00020; CAA77315.1; -.
 DR PIR; A01890; K2HURP.
 DR HSSP; Q99M37; 1191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 59 Complementarity-determining-1.
 FT DOMAIN 60 74 Framework-2.
 FT DOMAIN 75 81 Complementarity-determining-2.
 FT DOMAIN 82 113 Framework-3.
 FT DOMAIN 114 122 Complementarity-determining-3.
 FT DOMAIN 123 132 Framework-4.
 FT DISULFID 43 113 By similarity.
 FT NON TER 133 133
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

 Query Match 76.6%; Score 444; DB 1; Length 133;
 Best Local Similarity 76.8%; Pred. No. 1.4e-38;
 Matches 86; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

 QY 1 DIVMTQSPSLSPVIGPEPASISCRSSQSLQSGNNYLDWYLQKPGQSPQLLIYLGNSRA 60
 Db 21 DVMTQSPSLSPVTLGQFPASISCRSSQSLVYSDGNTYLNWYFQRFQSPRRLLIYKVSNRD 80

 QY 61 SGVPRDFSGSGGTDTLTKISRVEADVGIYCYMQALQIPLTFGGGTKEIK 112
 Db 81 SGVPRDFSGSGGTDTLTKISRVEADVGIYCYMQGTHTSWMTFGGTKEIK 132

 RESULT 11
 Q65ZC0 PRELIMINARY; PRT; 219 AA.
 ID Q65ZC0;
 AC Q65ZC0;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Kappa light chain C region (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c; TISSUE=Spleen;
 RX MEDLINE=96319505; PubMed=8768802;
 RA Kipp B., Schlaak M., Becker W.M.;
 RT "Cloning and expression of a recombinant mouse Fab-fragment
 RT recognizing a defined linear epitope of Chironomus thummi major
 RT allergen Chi t I."
 RL Int. Arch. Allergy Immunol. 110:348-353(1996).
 DR EMBL; Z37499; CAA85724.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.


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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW;  FACEDC3A3B03871D CRC64;

Query Match
Best Local Similarity 75.7%; Score 439; DB 2; Length 239;
Matches 83; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 21 DVVMTQSPSLPVLTPGQASISCRSTQSLVSDGNTYLNWFQRPQSPRLIYKVSNRD 80
QY 61 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112
Db 81 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112

RESULT 14
KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
TX TISSUE=Hybridoma; PubMed=6409088;
RA Chang J.-Y., Herbst R., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM578.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match
Best Local Similarity 74.0%; Score 429; DB 1; Length 113;
Matches 84; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

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Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYRMSNLA 60
QY 61 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112
Db 61 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112
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RESULT 15
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
TX TISSUE=Hybridoma; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.-Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
DR PIR; A01912; KVM517.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match
Best Local Similarity 73.6%; Score 427; DB 1; Length 113;
Matches 84; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYQMSNLA 60
QY 61 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112
Db 61 SGVPRFRSGSGSGTDFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112

Search completed: November 16, 2005, 22:01:55
Job time : 63.7941 secs
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 19.0441 Seconds
(without alignments)
439.017 Million cell updates/sec

Title: US-10-660-357A-38
Perfect score: 580
Sequence: 1 DIVMTQSPSLPVPICGPAS.....CMQALQIPLTGGGKVKVIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	92.4	113	3	US-09-025-769B-15
2	536	92.4	113	4	US-09-490-070A-15
3	536	92.4	113	4	US-09-490-153-15
4	536	92.4	113	4	US-09-490-324-15
5	533	91.9	112	4	US-09-254-180C-9
6	526	90.7	112	1	US-08-331-398A-49
7	526	90.7	112	2	US-08-331-397B-49
8	526	90.7	112	2	US-08-759-804A-49
9	526	90.7	112	3	US-09-227-693-49
10	521	89.8	112	3	US-09-240-274-30
11	519	89.5	113	1	US-08-082-623-4
12	515	88.8	114	3	US-09-025-769B-29
13	515	88.8	114	3	US-09-025-769B-45
14	515	88.8	114	4	US-09-490-070A-29
15	515	88.8	114	4	US-09-490-070A-45
16	515	88.8	114	4	US-09-490-153-29
17	515	88.8	114	4	US-09-490-153-45
18	515	88.8	114	4	US-09-490-324-29
19	515	88.8	114	4	US-09-490-324-45
20	515	88.8	281	3	US-09-025-769B-178
21	515	88.8	281	4	US-09-490-070A-178
22	515	88.8	281	4	US-09-490-153-178
23	515	88.8	281	4	US-09-490-324-178
24	512	88.3	239	4	US-10-000-489-8
25	510	87.9	112	3	US-09-000-088-2
26	509	87.8	108	1	US-08-488-113B-151
27	509	87.8	108	1	US-08-477-484B-151

28	509	87.8	108	1	US-08-107-669D-15	Sequence 15, Appl
29	509	87.8	108	1	US-08-472-788A-15	Sequence 15, Appl
30	509	87.8	108	2	US-08-477-531B-15	Sequence 15, Appl
31	509	87.8	108	2	US-08-646-360-151	Sequence 151, Appl
32	509	87.8	108	2	US-08-082-842A-15	Sequence 15, Appl
33	509	87.8	108	3	US-08-839-765-151	Sequence 151, Appl
34	509	87.8	108	3	US-09-136-389-151	Sequence 151, Appl
35	509	87.8	108	3	US-09-610-838-151	Sequence 151, Appl
36	509	87.8	108	4	US-09-711-485-151	Sequence 151, Appl
37	505	87.1	112	1	US-08-053-171-16	Sequence 16, Appl
38	504	86.9	112	1	US-08-478-039-88	Sequence 88, Appl
39	504	86.9	112	1	US-08-476-349A-88	Sequence 88, Appl
40	499.5	86.1	113	1	US-08-264-093-10	Sequence 10, Appl
41	491	84.7	100	4	US-09-472-087-115	Sequence 115, Appl
42	490	84.5	116	1	US-08-482-882-66	Sequence 66, Appl
43	490	84.5	116	1	US-08-483-389-66	Sequence 66, Appl
44	490	84.5	116	2	US-08-487-113D-66	Sequence 66, Appl
45	490	84.5	116	2	US-08-473-503-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-15

Query Match 92.4%; Score 536; DB 3; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.7e-46;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
; Sequence 15, Application US/09490070A
Db 1 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
; Sequence 15, Application US/09490070A
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112

RESULT 2

US-09-490-070A-15
; Sequence 15, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070A-15

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Best Local Similarity 92.0%; Pred. No. 1.7e-46;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112

RESULT 3

US-09-490-153-15
; Sequence 15, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-153-15

Query Match 92.4%; Score 536; DB 4; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.7e-46;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIVMTQSLPLVPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112

RESULT 4

US-09-490-324-15
; Sequence 15, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-324-15
Query Match 92.4%; Score 536; DB 4; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.7e-46;
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPKQSPQLLIYLGSNRA 60
Oy 61 SGVPRFSGSGGTDTFTLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 5
US-09-254-180C-9
Sequence 9, Application US/09254180C
Patent No. 6777540
GENERAL INFORMATION:
APPLICANT: OKUMURA, Ko
APPLICANT: EDA, Yasuyuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: USHIO, Yoshitaka
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
FILE REFERENCE: 050006-0055
CURRENT APPLICATION NUMBER: US/09/254,180C
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 271546/1996
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: 231472/1996

PRIOR FILING DATE: 1996-09-02
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-180C-9

Query Match 91.9%; Score 533; DB 4; Length 112;
Best Local Similarity 91.1%; Pred. No. 3.4e-46;
Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Oy 61 SGVPRFSGSGGTDTFTLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 6

US-08-331-398A-49
Sequence 49, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein

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; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human Igm antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match          90.7%; Score 526; DB 1; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 7
US-08-331-397B-49
; Sequence 49, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human Igm antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match          90.7%; Score 526; DB 2; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 8
US-08-759-804A-49
; Sequence 49, Application US/08759804A
; Patent No. 5950296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human Igm antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-759-804A-49

Query Match          90.7%; Score 526; DB 2; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;

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DB 1 DIVMTQSPSLPVTGPEPASISCRSSQSLQNGNNYLDWYLDYKQKQSQPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTLTKISRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 112
DB 61 SGVPDRFSGSGGTDTLTKISRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 112

RESULT 9
US-09-227-693-49
; Sequence 49, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/227,693
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-09-227-693-49

Query Match 90.7%; Score 526; DB 3; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLQNGNNYLDWYLDYKQKQSQPQLLIYLGSNRA 60
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DB 1 DIVMTQSPSLPVTGPEPASISCRSSQSLQNGNNYLDWYLDYKQKQSQPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTLTKISRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 112
DB 61 SGVPDRFSGSGGTDTLTKISRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 112

RESULT 10
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match 89.8%; Score 521; DB 3; Length 112;
Best Local Similarity 89.9%; Pred. No. 5.4e-45;
Matches 98; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 4 MTQSPSLPVTGPEPASISCRSSQSLQNGNNYLDWYLDYKQKQSQPQLLIYLGSNRAGV 63
DB 3 LTQSPSLPVTGPEPASISCRSSQSLQNGNNYLDWYLDYKQKQSQPQLLIYMGSNRAGV 62
QY 64 PDRFSGSGGTDTLTKISRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 112
DB 63 PDRFSGSGGTDTLTKINRVEADVGVIYCMQALQIPLTFGGGTRKVEIK 111

RESULT 11
US-08-082-623-4
; Sequence 4, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
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; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SDZ MSL 109"
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US-08-082-623-4

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Best Local Similarity 89.3%; Pred. No. 8.6e-45;
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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Db 1 DIVMTQSPLSPLVPVPGEPASISCRSSQSLHTNGYNYLDWYVQKPGQSPQLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112

RESULT 12
US-09-025-769B-29
; Sequence 29, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-025-769B-45

Query Match      88.8%; Score 515; DB 3; Length 114;
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-025-769B-29

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Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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QY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112
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RESULT 13
US-09-025-769B-45
; Sequence 45, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-025-769B-45

Query Match      88.8%; Score 515; DB 3; Length 114;
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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THE END OF THE LINE

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OM protein - protein search, using sw model

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Title: US-10-660-357A-38
Perfect score: 580
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	580	100.0	112	14	US-10-330-613-38
2	580	100.0	112	14	Sequence 38, Appl
3	580	100.0	112	16	US-10-330-530-38
4	552	95.2	112	14	US-10-660-357-38
5	552	95.2	112	14	Sequence 38, Appl
6	552	95.2	112	14	US-10-269-805-18
7	548	94.5	262	15	US-10-269-805-26
8	548	94.5	262	15	Sequence 26, Appl
9	547	94.3	112	15	US-10-309-762-33
10	545	94.0	112	15	US-09-880-748-2081
11	544	93.8	112	15	Sequence 2081, Ap
					Sequence 32, Appl
					Sequence 2, Appl
					Sequence 44, Appl

12	544	93.8	112	20	US-11-021-715-82	Sequence 82, Appl
13	544	93.8	112	20	US-11-021-715-85	Sequence 85, Appl
14	543	93.6	112	17	US-10-638-265-40	Sequence 40, Appl
15	543	93.6	112	17	US-10-638-265-48	Sequence 48, Appl
16	540	93.1	112	14	US-10-269-805-28	Sequence 28, Appl
17	540	93.1	112	16	US-10-663-244-71	Sequence 71, Appl
18	540	93.1	238	16	US-10-663-244-148	Sequence 148, Appl
19	539.5	93.0	111	14	US-10-041-860-16	Sequence 16, Appl
20	539.5	93.0	111	14	US-10-041-860-220	Sequence 220, Appl
21	539.5	93.0	111	14	US-10-041-860-254	Sequence 254, Appl
22	539.5	93.0	111	14	US-10-041-860-279	Sequence 279, Appl
23	539.5	93.0	111	16	US-10-665-383-12	Sequence 12, Appl
24	539	92.9	112	16	US-10-663-244-59	Sequence 59, Appl
25	539	92.9	112	16	US-10-638-265-60	Sequence 60, Appl
26	539	92.9	238	16	US-10-663-244-144	Sequence 144, Appl
27	538	92.8	112	15	US-10-292-088-103	Sequence 103, Appl
28	538	92.8	112	15	US-10-292-088-111	Sequence 111, Appl
29	538	92.8	112	17	US-10-877-773-30	Sequence 30, Appl
30	538	92.8	112	17	US-10-877-774-30	Sequence 30, Appl
31	538	92.8	112	17	US-10-735-916A-58	Sequence 58, Appl
32	538	92.8	113	15	US-10-308-817-177	Sequence 177, Appl
33	538	92.8	113	15	US-10-453-698-177	Sequence 177, Appl
34	538	92.8	125	14	US-10-010-942B-6	Sequence 6, Appl
35	538	92.8	125	15	US-10-388-389-6	Sequence 6, Appl
36	538	92.8	125	16	US-10-703-713-6	Sequence 6, Appl
37	538	92.8	125	16	US-10-704-070-6	Sequence 6, Appl
38	538	92.8	125	17	US-10-232-030-6	Sequence 6, Appl
39	537	92.6	112	15	US-10-292-088-112	Sequence 112, Appl
40	537	92.6	112	17	US-10-877-773-28	Sequence 28, Appl
41	537	92.6	112	17	US-10-877-773-31	Sequence 31, Appl
42	537	92.6	112	17	US-10-877-773-32	Sequence 32, Appl
43	537	92.6	112	17	US-10-877-773-33	Sequence 33, Appl
44	537	92.6	112	17	US-10-877-774-28	Sequence 28, Appl
45	537	92.6	112	17	US-10-877-774-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-330-613-38
; Sequence 38, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-38

Query Match	100.0%;	Score 580;	DB 14;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 7.6e-48;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DIVMTQSPSLPVPICPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLILYLSNRA	60	
Db	1	DIVMTQSPSLPVPICPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLILYLSNRA	60	
QY	61	SGVPRFRSGSGGTDTFLKISRVEADVGIYCMQALQIPLTFGGGKVEIK	112	
Db	61	SGVPRFRSGSGGTDTFLKISRVEADVGIYCMQALQIPLTFGGGKVEIK	112	
RESULT 2				

```
US-10-330-530-38
; Sequence 38, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-38

Query Match      100.0%; Score 580; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.6e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 3
US-10-660-357-38
; Sequence 38, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-38

Query Match      100.0%; Score 580; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.6e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 4
US-10-269-805-18
; Sequence 18, Application US/10259805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
```

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; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-18

Query Match      95.2%; Score 552; DB 14; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.7e-45;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 5
US-10-269-805-26
; Sequence 26, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-26

Query Match      95.2%; Score 552; DB 14; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.7e-45;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGIIYCMQALQIPLTFGGGTKVEIK 112

RESULT 6
US-10-309-762-33
; Sequence 33, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
```

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; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-33

Query Match
Best Local Similarity 95.2%; Score 552; DB 15; Length 112;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 60
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
DB 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112

RESULT 7
US-09-880-748-2081
; Sequence 2081, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match
Best Local Similarity 94.5%; Score 548; DB 10; Length 262;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 150 EIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 209
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
DB 210 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 261

RESULT 8
US-10-293-418-2081
; Sequence 2081, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
```

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; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2003-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2081

Query Match
Best Local Similarity 94.5%; Score 548; DB 15; Length 262;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 150 EIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 209
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
DB 210 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 261

RESULT 9
US-10-309-762-32
; Sequence 32, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-32

Query Match
Best Local Similarity 94.3%; Score 547; DB 15; Length 112;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 60
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
DB 61 SGVPRFSGSGSGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGKVEIK 112
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; Sequence 40, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-40

Query Match      93.6%; Score 543; DB 17; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.7e-44;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPSLSPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db      1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYKYLEWYLOKPGQSPQLLIYLGSNRA 60

Qy      61 SGVPRFSGSGSGTDFTLKISRVEADVGIIYCMQALQIPLTFGGGTVKEIK 112
Db      61 SGVPRFSGSGSGTDFTLKISRVEADVGIIYCMQALQIPLTFGGGTVKEIK 112

RESULT 15
US-10-638-265-48
; Sequence 48, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-48

Query Match      93.6%; Score 543; DB 17; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.7e-44;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPSLSPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db      1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYKYLEWYLOKPGQSPQLLIYLGSNRA 60

Qy      61 SGVPRFSGSGSGTDFTLKISRVEADVGIIYCMQALQIPLTFGGGTVKEIK 112
Db      61 SGVPRFSGSGSGTDFTLKISRVEADVGIIYCMQALQIPLTFGGGTVKEIK 112

Search completed: November 16, 2005, 23:05:45
Job time : 68.7647 secs
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